

ID	Score	Query		DB	ID	Description
		Match	Length			
1	694.2	61.9	2754	1	US-08-196-989B-1	Sequence 1, Appli
2	694.2	61.9	2754	1	US-08-760-936-1	Sequence 1, Appli
3	307	27.4	1137	3	US-09-082-088-1	Sequence 1, Appli
4	268	23.9	2232	1	US-08-196-989B-3	Sequence 3, Appli
5	268	23.9	2232	2	US-08-760-936-3	Sequence 3, Appli
6	195	17.4	1637	2	US-08-852-824-3	Sequence 3, Appli
7	187.6	16.7	1649	2	US-08-845-566-2	Sequence 2, Appli
8	139.8	12.5	2250	3	US-08-763-938-1	Sequence 1, Appli
9	138.2	11.6	1761	3	US-08-789-982-1	Sequence 1, Appli
10	130.2	11.6	1861	3	US-08-861-747-1	Sequence 1, Appli
11	130.2	11.6	1889	3	US-08-861-747-3	Sequence 3, Appli
12	125.4	11.2	1875	5	PCT-US96-1061B-1	Sequence 1, Appli
13	118.6	10.6	1065	4	US-09-325-897-1	Sequence 1, Appli
14	118.6	10.6	1356	3	US-08-997-803-13	Sequence 13, Appl
15	118.6	10.6	1523	3	US-08-997-803-12	Sequence 12, Appl
16	93.8	8.4	1338	2	US-08-044-812A-3	Sequence 3, Appli
17	93.8	8.4	1338	2	US-08-475-637-3	Sequence 3, Appli
18	93.8	8.4	1338	3	US-08-706-281A-11	Sequence 11, Appl
19	93.8	8.4	1338	4	US-09-191-359-3	Sequence 3, Appli
20	93.8	8.4	1338	4	US-09-097-231-11	Sequence 11, Appl
21	93.8	8.4	2185	2	US-08-467-948A-3	Sequence 3, Appli
22	93.8	8.4	2185	3	US-08-467-947A-3	Sequence 3, Appli
23	90	8.0	639	3	US-08-997-803-3	Sequence 3, Appli
24	89.4	8.0	1080	1	US-08-671-525B-5	Sequence 5, Appli
25	89.4	8.0	1080	1	US-08-672-109B-5	Sequence 5, Appli
26	89.4	8.0	1080	1	US-08-842-045-5	Sequence 5, Appli
27	89.4	8.0	1080	2	US-08-842-238-5	Sequence 5, Appli

	Query Match	61.98;	Score 694.2;	DB 1;	Length 2754;
	Best Local Similarity	82.2;	Pred. No. 1.4e-146;		
	Matches 811;	Conservative 0;	Mismatches 173;	Indels 3;	Gaps 1
Qy	136	gccatgcaggagacgacctccgcgcaggtggcctcgccgtccatcgatcatctctgttc	195		
Db	223	GACATGCAGGAGAGCCCTCCGCAAGTGGCTCGCCCTCATCATCATTTATGCTGT	282		



QY 676 gtggccctgtacgtgcacatactactggtggtgcgcctcaagccacgcgtgacatggccgc 735  
DB 763 GTGGCCCTGTACGTCGCAATCTACTGCTAGTCCGCTCAAGCCCATGCGGAGCTTCTGCTGGT 822  
QY 736 ccgcagacgttagccctgcctcaagcagcgtaccacgtgctagggcgtctttatgctgc 795  
DB 823 CCTCAGACGCTGGCCCTGCTCAAGACAGTCAACATCGTACGTTGGGTGTTTTCATCATCTGC 882  
QY 796 tggctgcgccttcagacatactctcttggaactatgctgtcccgctccactccctgcgcg 855  
DB 883 TGGCTGCGGCTTTTAGCATCTTCTTAGACTCTACTGTCGCTCCGCTCCGGCCCTGCTCT 942  
QY 856 atcctctacaaagccacatacttttgcgcgtctccacccctgaattccctgctcaacccc 915  
DB 943 GTCCCTACAAAGCCATTATTCTTTGCTTCGCGCACCCCTCAACTCTGTGCAACCCCT 1002  
QY 916 gtcattacacgtggcgcagcgggacgtgcgcgggaggtgcttcggccgctgcagtcg 975  
DB 1003 GTCATCTATACATGGCGTAGCGGACCTTCGGAGGGAGGTACTGAGGCCCTGCTGTGC 1062  
QY 976 tggcggccgggggtgggggtgcagggacggagggcgggtgctgggaccccgccacacccc 1035  
DB 1063 TGGGGGAGGGGAGGAGGACACAGGCGCA--GAGGTGGGAACCTTGGTCAACGACTC 1119  
QY 1036 ctgcactccgcagctccagctccctggagaggggagcagtcacatgccccacgtcaccacg 1095  
DB 1120 CTGCCCTCCGAGCTCCAGCTCCCTGGAGAGAGGCTTCATATGCTCATATGCTCAATCGCCA 1179  
QY 1096 tttctggagggcaacacagtggtctga 1122  
DB 1180 TTTCTGGAGGGCAACACAGTGTGCTGA 1206

RESULT 3

US-09-082-088-1  
; Sequence 1, Application US/09082088  
; Patent No. 6130067  
; GENERAL INFORMATION:  
; APPLICANT: TSUI, PING  
; TITLE OF INVENTION: HUMAN EDG3sb GENE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/082,088  
; FILING DATE: 20-MAY-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GP-70453  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1137 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-082-088-1

Query Match 27.4%; Score 307; DB 3; Length 1137;  
Best Local Similarity 61.0%; Pred. No. 3.8e-60;  
Matches 520; Conservative 2; Mismatches 319; Indels 12; Gaps 1;

QY 156 ccgcaggtggcctcgcccttcactcctctctgttgccactgtggtggaacacct 215  
DB 114 CAGCAGCTCACACACGCTGCTTCTTGGTCATCTCAGCTTCATCGTCTTGGAGAACCT 173  
QY 216 tctggtgctcattgctgggtggccgaaacagcaagttccactcctggcaatgacctgttct 275  
DB 174 GATGGTTTGTATGGCCATCTGGAAACAAATAATTAATTCACACCGCATGTACTTTTCAT 233  
QY 276 gggcaacctggccgctccgactactgagcagcgtggccttcgttagccaatadddtgc 335  
DB 234 TGGCAACCTGGCTCTCTGGGACCTGCTGGCGCATCGCTTACAAGGTCAACATTCAT 293  
QY 336 ctctgctctgtcaagcgtgaggtgacgctgtgcaagttgttgcggcggagggctctgc 395  
DB 294 GTCTGCAAGAGACGCTTACGCTGTCTCCACGCTGTGGTTCTTCAGGGAGGCGAGTAT 353  
QY 396 ctccatacagctctcgccctctgtcttcagcctcctgcccactcctgcccactgagccacgt 455  
DB 354 GTTCGTGGCCCTTGGGGCGTCCACCTGACCTTACTGGCCATCGCCATCGAGCGGACTT 413  
QY 456 ggcattggcaaggtcaagctgtatggcagcagcaagcgtgcgcagctgctctgctcat 515  
DB 414 GACAATGATCAAAATGAGGCTTTACGAGCGCCAAACAGAGGACCGCGCTCTCTCTCTGAT 473  
QY 516 cggggcctcggtgctcactcctgctggtgctggtggtggtggtggtggtggtggtggtggt 575  
DB 474 CGGGATGCTGCTGCTCATTTGCTTTCAGCTGGCGCCCTGCCCCATCTTCTGGGTGGAACGT 533  
QY 576 cctgggcaactcgtgctcactgctcactgctcactcctcctcctcctcctcctcctcctcct 635  
DB 534 CCTGCACATCTCCCTGACTGCTTACCATCTCGCCCTCTACTCCAAAGAGTACATTCG 593  
QY 636 gtgctggtgacacatctctccatcctctgttgccatcgtggccctgtacgtgcgcac 695  
DB 594 CTTCTGCATCAGCATCTTACGGGCCATCTCTGCTGACCATGCTGATCTCTTACGCGCAT 653  
QY 696 ctactggtggtccgctcaagccacgctgacatggccgccc-----cgcadac 743  
DB 654 CTACTTCTGCTGAAGTCCACGACGCGCTAAGTGGCCCAACCAACAACATCGGAGCGGTC 713  
QY 744 gctagccctgctcaagacggttcacacatcgtgctgaggtcttcttctgctgctgctgctgct 803  
DB 714 CATGGCACTGCTGGGACCGTGGTATTTGCTGAGCGCTGTTCATCGCTGCTGCTGCTGCTGCT 773  
QY 804 cgccttcagacatacctcttggactatgctgctgctcctcctcctcctcctcctcctcctcctc 863  
DB 774 ACTCTTCATCTCTTCTCTCATTTGATGTGGCCTTGCAGGTGAGGGGTGCGGCGTCCCTCTT 833  
QY 864 caaagccactactcttctcgcgtctccacccctgaatccctgctcaccctgctcaccctgctcctc 923  
DB 834 CAAGGCTCAGTGGTTTCATCTGTTGGCTGTGCTCAACTCCGCCCATGAAACCCGGTCACTA 893  
QY 924 cactggtgcgcagccgggacacctgcggggaggtgcttgcgcgctgcagtgctgctgctgctgct 983  
DB 894 CACGCTGGCCAGCAAGAGATGCGCGGCGCTTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 953  
QY 984 ggggggtgggggtg 996  
DB 954 CAGGGGACGGGGG 966

RESULT 4  
US-08-196-989B-3





```

; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 269..1420
US-08-760-936-3

```

Query Match 23.9%; Score 268; DB 2; Length 232;  
Best Local Similarity 58.3%; Pred. No. 2.4e-51;  
Matches 508; Conservative 2; Mismatches 329; Indels 33; Gaps

[illegible]

RESULT 6

```

US-08-852-824-3
; Sequence 3, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1201)
; US-08-852-824-3

```

Query Match 17.4%; Score 195; DB 3; Length 1637;  
Best Local Similarity 54.2%; Pred. No. 4.5e-35;  
Matches 467: Conservative 2; Mismatches 374; Indels 1

[illegible]



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,938
FILING DATE: 12-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: P8074-6018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
-08-763-938-1

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Query Match 12.5%; Score 139.8; DB 3; Length 2250;  
Best Local Similarity 51.0%; Pred. No. 1.1e-22;  
Matches 326; Conservative 2; Mismatches 311; Indels 0;

136	gccaatgcaggagacgacctccgccaggtggcctcggcccttcatcgtcaactcctctgtgc	195
Qy		
137	gccaatgcaggagacgacctccgccaggtggcctcggcccttcatcgtcaactcctctgtgc	
Db		
351	gccacagaattggaacacacatgagcaacagctggatggagactggccatcattgtttgcgng	410
Qy		
196	gccatgtggttgaaacacctctgggtgctcattgcggtggcccgaaacagcaagttccac	255
Db		
411	ttcatcatgttgcccaattctccctgggtcatgtggggcaattctacgtcaacgccgcgtccat	470
Qy		
256	tcggcaatgtacactgtttctgggcaaccttggccgctccgatctactcggcagcgctggcc	315
Db		
471	ttcccattttatttacttgatggccaacctggctgctgcagacttcttcgctggattggcc	530
Qy		
316	ttcgtagccaataadtttgcctctcgtcgtgctcagctgagcgtgagcgcctgtgcagtgg	375
Db		
531	tactttcacctgtatgttcaatacagagaccttaatacccgagagactgactgtttagcacgtgg	590
Qy		
376	tttgcggcgaggcctctgcctccatcaagcctctggcctctgtcttcagcctccctggcc	435
Db		
591	ctcctccggcaggccctcattgacaccagcctgacagcttctgtgtgccaaacctgtcgct	650
Qy		
436	atcgccattgagcgccacgttggccaattgcgaaggtcaagctgtatggcagcgacaagaagc	495
Db		
651	attgtctatcagagaggcacatcacgggttttccgcatgcagctccatcacgaatgagcaac	710
Qy		
496	tgcgcatgctctctgcatacggggcctcgttgctcatctcgtctggtctcgtcgtggccg	555
Db		
711	cgccgctgggtgggtgattgtagtcacttgacactatggcccaattgtgatgggtgctata	770
Qy		
556	cccatccttgctggaactgcctggccacctggagcctgtccactgtccctgcctctc	615
Db		
771	cccaagtggcctggaaactgcactctgtgatattcgatcactgtttccaacatggcacccctc	830
Qy		
616	taagccaagcattatgtcgtgtgcgtggtgacctatcttccatcatcctgttggccatc	675
Db		
831	tacagtgacttccacttagtcttcttgggccatttttcaacctgggtgacctttgttgggtcatg	890
Qy		
676	gtggccctgtacgtgcgcatactactcgttgctgcgtctcaagccacgctgacatggccgcc	735
Db		
891	gtggttctctacgcctcacatcttttggctatgtttcgccagaggactatgaggatgtctcgg	950
Qy		
736	ccgcagacgtatagcctctgtcgaagaoggtcaccatcgtg	774
Db		
951	catagttcttgaccacccaggaggaattcgggacaccatcatgatg	989
Qy		

## RESULT 9

RESULT 9  
US-08-789-982-1

US-06 789 982 1  
; Sequence 1, Application US/08789982

Patent No. 6037146  
GENERAL INFORMATION:  
APPLICANT: Sathe, Ganesh  
APPLICANT: Bergsma, Derk  
TITLE OF INVENTION: CDNA CLONE HECH90 THAT ENCODES  
TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,982  
FILING DATE: 28-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: ATG50050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
S-08-789-982-1

[illegible]



STREET: 655 15th St., NW, Suite 330 - G Street Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/861.747  
APPLICATION NUMBER: 536  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Jahns, Kristina M.  
REGISTRATION NUMBER: 41,092  
REFERENCE/DOCKET NUMBER: P8074-7003  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1889 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-861-747-3

Query Match 11.6%; Score 130.2; DB 3; Length 1889;  
Best Local Similarity 49.9%; Pred. No. 1.4e-20;  
Matches 403; Conservative 2; Mismatches 372; Indels 30; Gaps 2;

```
QY 203 tggtagaaacctctgtgctcattgcggtggccggaacagcaagtccactcggcaa 262
DB 316 TGTGACCAATCTGTGTCTATAGCAGCATCGCTCCCAACCGCGCTTCCACACGCCCA 375
QY 263 tgaacctgtttctgggaacatggccgctcgcattcctactcggcagcgctggcctcgtag 322
DB 376 TCTACTACCTGCTCGGCAATTCGCGCGGCTGACCTCTTCGCGGGCGTGGCTACCTCT 435
QY 323 ccaatadttgtctctgtcctgtcacgctgagcgtgacccctgtcagtggttggcc 382
DB 436 TCCTCATGTTCCACTGCTGCCGACAGCCGCGACTTTCATTGAGGCGTGGTTCCTGCG 495
QY 383 gggagggtctgtcctccatcacgctctcggcctctgtcttccagcctcctggccatcgcca 442
DB 496 GGCAGGGCTTGTGTGACACAAAGCTCACTGCTGGTGGCCACACTGCTGGCCATCGCG 555
QY 443 ttgagcgcacgtggccattgccaaagttcaagctgtatggcagcagacagagctgccga 502
DB 556 TGSAAACGGCAGCGAGTGTGATGCGCGTACAGTTTCACAGCGCGCTGCCCGTGGCCGCG 615
QY 503 tgcctctgtcattcggggtcgtggtcctcctcgtcgtgctcgtggtggtcgtggtcgtc 562
DB 616 TGGTCACTGCTCATTTGTGGCGCTGTGGTGGCTGCGCTGGCGCTGGGCTGTTCCTGCCC 675
QY 563 ttggctggaactgctggggtcctcagggcctcagggcctcctcgtcgtcctcctcagcca 622
DB 676 ACTCTGCGCACTGCTCTGTGCTGCTGGACCGCTGCTACGCACTGCGACCCCTGCTCAGCC 735
QY 623 agcattatgtcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 682
DB 736 GCTCCTATTTGGCGCTGTGGGCTGTGTCAGCGCTGCTTGTCTTCTGCTCATGTTGGTGTG 795
QY 683 tgaacgtgcatcattcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 736
DB 796 TGTACACCCGATTTTATATATATATATATATATATATATATATATATATATATATATAT 855
QY 737 -----cgagacgctagcctcgtcgaagcgttcacccatcgtgc 775
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DB 856 GCTGCCACCCCGCTACCGAGAGACACCGCTCAGCCTGGTCAAGACTGTTGTCTATCATCC 915
QY 776 taggggtcttctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 835
DB 916 TGGGGGCGTTCGTGGTCTCTGGACACAGCCAGGTGGTGTCTGCTCTGCTCTGCTCTGCT 972
QY 836 gtccggtccactcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 895
DB 973 TAGGCTGTGAGTCTCTGCAATGCTCTGCTGTAGAAAAGTACTTCCCTACTCTTGGCCGAG 1032
QY 896 tgaattcctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 955
DB 1033 CCAACTCACTGCTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1092
QY 956 tgcttcggcgcgtgcaagtgtgctgctgctgctgctgctgctgctgctgctgctgctgct 982
DB 1093 TCCGGCGCTTCTCTGCTGCGGTGCC 1119
```

## RESULT 12

PCT-US96-10618-1  
Sequence 1, Application PC/TUS9610618  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Guegler, Karl J.  
APPLICANT: Au-Young, Janice  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOGY  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10618  
FILING DATE: 20-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,352  
FILING DATE: 20-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/567,817  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Glastier, Debra J.  
REGISTRATION NUMBER: 33,888  
REFERENCE/DOCKET NUMBER: PF-0042 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1875 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: Rheumatoid Synovium  
CLONE: 80853  
PCT-US96-10618-1

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Human
; US-09-325-897-1

Query Match      10.6%; Score 118.6; DB 4; Length 1065;
Best Local Similarity 52.1%; Pred. NO. 4.8e-18;
Matches 261; Conservative 2; Mismatches 238; Indels 0; Gaps 0;

QY 199 attgtggtggaagaacctttctgtgtcattgcggtgcccgcgaacacagacagttccactgc 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 attttttttctaattctctgttcacgcgcgagtgatcaaaaacagaaaatttcatttc 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 259 gcaatgatactgtttctgvgcaacctggccctccgactctactgcgagcggtggccttc 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 cccctctactaccctgttgtaatttagctgctgcggaattcttcgcgtgaatgccttat 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 319 gtagcgaataddttgtctctctgtgcctgtcacgtgaggtgcagcctgtgcagtgttt 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 gtattctgatgtttaacacagcccagtttcaaaaactttgactgtcaaacgctggttt 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 379 gcccgggagggtctgctctccatcaacgtctcggcctctgtcttcagcctctggccatc 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 ctccgtcagggtctctggacagttagctgttgccttccctcaacactgctgtgtttac 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 14
US-08-997-803-13
; Sequence 13, Application US/08997803
; Patent No. 6057126
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: GUPTA, Ashwani
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
; TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street, N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,803
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Wong, King L.
: REGISTRATION NUMBER: 37,500
: REFERENCE/DOCKET NUMBER: P8074-7020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1356 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: -08-997-803-13

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Query Match	10.6%	Score 118.6	DB 3	Length 1356
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RESULT 15
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; Sequence 12, Application US/08997803
; Patent No. 6057126
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: GUPTA, Ashwani
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VIAS, Tejpal B.
; TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
; NUMBER OF SEQUENCES: 15

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CORRESPONDENCE ADDRESS:  
ADDRESSER: Nikaïdo, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street, N.W., Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997.803  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wong, King L.  
REGISTRATION NUMBER: 37,500  
REFERENCE/DOCKET NUMBER: P8074-7020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1523 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 261..1322  
US-08-997-803-12

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Best Local Similarity	52.1%	Pred. No. 5.2e-18			
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

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Run on: December 20, 2001, 10:06:41 : Search time 2907.25 seconds  
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6366.785 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.ov.\*
- 5: gb.pat.\*
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- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
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- 13: gb.un.\*
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- 15: em.ba.\*
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- 33: em.htg.hum.\*
- 34: em.htg.inv.\*
- 35: em.htg.rod.\*
- 36: em.htg.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

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2	984	87.7	156503	9	AC011511	AC011511 Homo sapi
3	710.2	63.3	1059	10	AF108020	AF108020 Mus muscu
4	708.6	63.2	214006	2	AC073775	AC073775 Mus muscu
5	708.6	63.2	220103	2	AC073781	AC073781 Mus muscu
6	697.4	62.2	1139	6	E07989	E07989 DNA encodin
7	697.4	62.2	1139	10	AB016931	AB016931 Rattus no
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16	383.6	34.2	1110	5	AF260256	AF260256 Danio rer
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18	314.2	28.0	978	10	AY011714	AY011714 Myocastor
19	313.4	27.9	978	10	AY011704	AY011704 Muscardin
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22	308.6	27.5	1137	6	AX085542	AX085542 Sequence
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24	307	27.4	1137	6	AR112475	AR112475 Sequence
25	300.6	26.8	978	10	AY011708	AY011708 Hystrix b
26	297.8	26.5	978	4	AY011737	AY011737 Tapirus i
27	296.4	26.4	978	4	AY011717	AY011717 Ochotona
28	296.2	26.4	978	9	AY011720	AY011720 Lemur cat
29	294.2	26.2	975	4	AY011739	AY011739 Leopardus
30	293.2	26.1	978	4	AY011697	AY011697 Procavia
31	292.6	26.1	975	4	AY011738	AY011738 Fells cat
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ALIGNMENTS

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VERSION	AF034780.1	GI:4090955				
KEYWORDS	human.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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AUTHORS	MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.					
TITLE	Cloning and characterization of a putative G-protein coupled receptor potentially involved in development					
JOURNAL	Mol. Cell. Neurosci. 5 (3), 201-209 (1994)					
MEDLINE	94373324					
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AUTHORS	An,S.					
TITLE	Edg5, a Human homolog of rat H218 that is a functional receptor for					

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lysophingolipids
Unpublished
REFERENCE 3 (bases 1 to 1062)
AUTHORS An,S.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
Ave., San Francisco, CA 94143-0711, USA
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lysophingolipids
Unpublished
REFERENCE 3 (bases 1 to 1062)
AUTHORS An,S.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
Ave., San Francisco, CA 94143-0711, USA
FEATURES
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BASE COUNT 166 a 367 c 294 g 235 t
ORIGIN

Query Match 88.1%; Score 988.8; DB 9; Length 1062;
Best Local Similarity 94.5%; Pred. No. 6.4e-162;
Matches 1060; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 atggcgagctgttactcggagtagctacccaacccaacgaaggtccaggaaactataattat 60
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Qy	256	tcggcaaatgaactgtttcttgaggaaacctggccgacctccgatactactagggaaggctagcc	315
Db	196	TGAGCAATATGACTGTTCCTTGGCAACTGGCAGCCTGACCTGCTGGGAGGGGTGGCC	255
Qy	316	ttcgtagcaaataddttgctctcttgctctgttcacgctgaggctgagcgcctgtcagctgg	375
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Qy	376	tttgccccggagggtctgctccatcaatcaogctctctggcctctgttcttaagcctctggcc	435
Db	316	TTTGCCCGAGAGGTCTCCGCCCTTCATCAGCTCTCCGCTCGGCTCTTAGCCTCTCGGCC	375
Qy	436	atcgccattgagcgccagctggccattgccaaaggtccaagctgtatggcagcgacaagc	495
Db	376	ATCGCCATCGAGAGACAAGTGGCCCTCGCCAAAGTCAAGCTCTACGGCAGTGCACAAAGC	435
Qy	496	tgcgcgcatcttctgctcactcggggccctcgtagctcatctcgctggctcctcgtaggcctg	555
Db	436	TGCGGAATGCTGATGCTCATCGGGCCTCTTGGCTGATATCGCTGATTCTGGTGGGCTTG	495
Qy	556	ccatccttgctggaactgctggggccacctcgaggcctgctccactgctcctcctctctc	615
Db	496	CCCATCCTGGGCTGGAAATTTGCTGAACCAAGCTTGAAGGCGCTGCTCCACGCTGCCCTC	555
Qy	616	tacgccaagcattatgtgctgtgcgtggtgacacattcttccatcactctgttggccatc	675
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Qy	676	gtggccctgtacgtgcgcactactctactgctggttgcctcgaagccacgctgacatggccgc	735
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Qy	736	cgcgacagctagccctgctcgaagcgtgcacactcgtgctaggcgtcttatcgtctgc	795
Db	676	CCTCAGACGCTAGCCCTGCTCAAGACGCTCACCATCGTACTTGGGTGTTTTCATCATCTGC	735
Qy	796	tggctgcgcgccttcgaactcctcctcttgagatagctgtcccgctccactcctgcctgc	855
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Qy	856	atcctctcaaaagcccaactacttttgcgcgtctccacctgaattcctgctcaacccc	915
Db	796	GTCTCTCTACAAAGCCACATATTTTTTGGCTTTGGCCACCCCTTAACTCACTGCTCACTCT	855
Qy	916	gtcatctacagtggcgagccggagacctggcggggaggtgcttcggcgctgcagctgc	975
Db	856	GTCACTATACGTGGCGTTAGCGGGACCTTTCGGAGGGAGGTGCTGCGGCCCTCTCAGTGC	915
Qy	976	tggcgccgggggtgggggtgcgaagacggaggcggttcgggaaccccgggccacacactc	1035
Db	916	TGGCGGAGAGGAAGGAGGTGACGGGAGCGCA---GAGGTGGGAACCCCTGGTCAACCGACT	972
Qy	1036	ctgcccactccgagctccagctccctggagaggggcatgacatgcccacgtccaccacg	1095
Db	973	CTGCCCTCCGAGCTCCAGCTCCCTGGAGAGAGCATGCAATATGCTATACATCACCGACA	1032
Qy	1096	ttcttgaggggcaacacggtggtctga	1122
Db	1033	TTTCTGGAGGTTAACACAGTGTCTGA	1059

WILLIAM

RESULT:  
AC073775

AC073775  
LOCUS  
AC073775 214006 bp  
DNA

५८

AC073775 214006 bp DNA HTG 18-JUL-2000  
Mus musculus clone RP23-382B11, WORKING DRAFT SEQUENCE, 9 ordered  
pieces.

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AC073775
AC073775.2 GI:9256790
HTG: HTGS_PHASE2; HTGS_DRAFT.
SOURCE:
house mouse.
ORGANISM:
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 214006)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 214006)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810392.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1883595
Center clone name: RPCI-23_382B11
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Summary Statistics
Consensus quality: 209197 bases at least Q40
Consensus quality: 212478 bases at least Q30
Consensus quality: 212996 bases at least Q20
Estimated insert size: 218930; agarose-fp estimation
Estimated insert size: 213656; sum-of-contigs estimation
Quality coverage: 9.1 in Q20 bases; agarose-fp estimation
Quality coverage: 9.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1
11489: contig of 11489 bp in length
11490
11589: gap of unknown length
11590
72347: contig of 60758 bp in length
72348
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79269: contig of 6822 bp in length
79270
79369: gap of unknown length
79370
79945: contig of 576 bp in length
79946
80045: gap of unknown length
80046
101339: contig of 21294 bp in length
101340
101439: gap of unknown length
101440
118105: contig of 16666 bp in length
118106
118205: gap of unknown length
118206
142604: contig of 24399 bp in length
142605
142704: gap of unknown length
142705
151311: contig of 8607 bp in length
151312
151411: gap of unknown length
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214006: contig of 62595 bp in length.
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49780 a 52378 c 54716 g 56332 t 800 others
BASE COUNT
ORIGIN

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Query Match
Best Local :
Matches 82
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63.2%;	Score 708.6;	DB 2;	Length 214006;
83.1%;	Pred. No. 4.8e-114;		
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1. .220103
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LOCUS		E07989				
DEFINITION		DNA encoding a peptide that has receptor activity coupling with GTP-binding protein.				
ACCESSION		E07989	1	GI:2176120		
VERSION		JP 1994234797-A/1.				
KEYWORDS		Homo sapiens.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1 (bases 1 to 1139)				
AUTHORS		Takuwa,A..				
TITLE		NEW PEPTIDE HAVING RECEPTOR ACTIVITY AND DNA ENCODING THE PEPTIDE				
JOURNAL		Patent: JP 1994234797-A 1 23-AUG-1994;				
COMMENT		TSUMURA & CO, TAKUWA AKIRA OS Homo sapiens (human) PN JP 1994234797-A/1 PD 23-AUG-1994 PF 10-FEB-1993 JP 1993044330 PI TAKUWA AKIRA PC C07K13/00,C07H21/04,C12N15/12,C12P21/02; CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers FH FT source 1..1139 /organism='Homo sapiens' FT CDS 37..1095 /product='a peptide that has receptor activity FT coupling FT with GTP-binding protein'. FT Location/Qualifiers 1..1139 /organism='Homo sapiens' /db_xref='taxon:9606'				
BASE COUNT		210 a	359 c	295 g	275 t	
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Best Local Similarity		82.4%;	Pred. No. 1.8e-111;			
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Db	112	GACATGCAGGAGAGCGCCCTCCCGCAGGTGGCCCTCCGCCCTTCATCATCATTTTATGCTGT	171			
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Qy	376	tttgccggaggagctctgctccatcaacgctctcgccctctgttcttaagcctcctgccc	435			
Db	352	TTTCCCGGAGAGGGTTTCAGCTTTCATCAGCTCTCTGCCTCGGCTTTCAGCTCTCTGGCC	411			
Qy	436	atcgccattgagccacgtagccattcccaaggtccaagctgtatgcagcagcaagaac	495			







[illegible]





## RESULT 13

AF289992 607 bp mRNA ROD 02-AUG-2001  
LOCUS Cavia porcellus endothelial differentiation sphingolipid  
DEFINITION G-protein-coupled receptor 5 mRNA, partial cds.  
ACCESSION AF289992  
VERSION AF289992.1 GI:15077230  
KEYWORDS domestic guinea pig.  
SOURCE Cavia porcellus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
REFERENCE 1 (bases 1 to 607)  
AUTHORS Segura,B.J., Xiao,L., Cowles,R.A., Turner,D.J., Logsdon,C.D. and Mulholland,M.W.  
TITLE Sphingosine-1-phosphate Mediates Calcium Signaling in Enteric Glia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 607)  
AUTHORS Xiao,L. and Mulholland,M.W.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-2000) Surgery, University of Michigan, 1500 E. Medical Center Drive, Ann Arbor, MI 48109-0331, USA  
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BASE COUNT 79 a 214 c 184 g 130 t  
ORIGIN

Query Match 41.9%; Score 470.6; DB 10; Length 607;  
Best Local Similarity 87.4%; Pred. No. 4.1e-72;  
Matches 515; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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Db 19 GACGTGCGGGAGACACGTCGCCGACGAGTGGCTCGGCTTCATCGTCATCGTCTGC 78  
C 196 gccattgtgtggaacaccttctgtctcattgctcattgctggtggccgaacagttccac 255  
Db 79 GCCATCGTGGTGGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 138  
Qy 256 tcggcaatgtaacctttcttctgggaacacgtggcgcctcgcattactgagcggctggccc 315  
Db 139 TCGGCATGTATCTCTTCTCGGGAACCTTGGCGGCTCGGACCTCGGCGGCTGGCC 198  
Qy 316 ttctgagcaataddttctctgtcctgtcagctgagctgagctgagctgagctgagctg 375  
Db 199 TTTCATCGGCAACACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258  
Qy 376 ttgtcccgaggaggtctgtcctccatcacgctctcgtcctcgtctgtctcagctcctggcc 435  
Db 259 TTCGCGCGGAGGGCTCGGCTTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318  
Qy 436 atcgccattgagcgcaacgtggccattgccaagggtcaagctgatatggcagcgaagagc 495  
Db 319 ATCGCCATCGAGCGGACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 378  
Qy 496 tgcgcattctctctcaggggctggtggtcattcgtcattcgtcattcgtcattcgtcattcgt 555

Db 379 TCCGCCATGCTGCTCTCATCGGGCCCTCATGGGTCATGCTTCTGCTGGTCTGGCGGCTTC 438  
Qy 556 cccatcttgctgaactgcttgccacccctgagggctgctccactgctcctgctctc 615  
Db 439 CCCATCCCTGGGCTGGAACCTGCTGGGGCGCCCTGGACACCTGCTCCACTGCTGCTGCCCTC 498  
Qy 616 tacgccaagcattatgtgctgctggtgacccattcttccatcatcctgctgtggccatc 675  
Db 499 TAGCCCAAGCAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 558  
Qy 676 gtggccctgtacgtgcgcatctactgctggtgctccctcaagcagcgtg 724  
Db 559 GTGGTCTTGTAGTCCGATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607  
RESULT 14  
AF090995 573 bp mRNA ROD 19-OCT-2000  
LOCUS Rattus norvegicus putative G-protein coupled receptor (GPCR18)  
DEFINITION mRNA, partial cds.  
ACCESSION AF090995  
VERSION AF090995.1 GI:10880457  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 573)  
AUTHORS Carroll,S.L., Miller,M.L. and Benedict-Hamilton,H.M.  
TITLE Identification and characterization of novel G-protein coupled  
receptors expressed in regenerating peripheral nerve  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 573)  
AUTHORS Carroll,S.L., Miller,M.L. and Benedict-Hamilton,H.M.  
TITLE Direct Submission  
JOURNAL Submitted (11-SEP-1998) Pathology, University of Alabama at  
Birmingham, LHRB513, 701 South 19th Street, Birmingham, AL  
35294-0007, USA  
FEATURES Location/Qualifiers  
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Qy 400 atcacgctctcggcctctgtcttccagcctcctgcccattgagcgcacagtgagcc 459  
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Db 122 ATCCCAAGGTCAGAGCTCTACGGAGTGCACAAAAGCTGTGCAATATTGATGCTCATTTGGG 181
QY 520 gctcgtggtcattctcgtggtctcgtggtggtggtggtggtggtggtggtggtggtggtg 579
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Db 182 GCCTCTTGGCTGATATCGCTGATCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 241
QY 580 ggcacactgagggcctgctcctcctcctcctcctcctcctcctcctcctcctcctcctc 639
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Db 302 GTGCTACCAATCTCTCTGTCATCTACTTGGCTATCGTGGCTTGTAGCTCCGAATCTAC 361
QY 700 tgcgtggtccgcctcaagccagcgtgacatgcccgcgcgcgcgcgcgcgcgcgcgcgcgc 759
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Db 542 TTTGCCCTTCCGCCCTCAACTCTCTGCTCAA 573

RESULT 15
MUSGPCR13      540 bp      mRNA      ROD      17-MAR-1994
LOCUS          Mouse EDG-like receptor mRNA, partial cds.
DEFINITION     L20334
ACCESSION      L20334.1  GI:438786
VERSION        EDG-like receptor.
KEYWORDS       Mus musculus cDNA to mRNA.
SOURCE         Mus musculus
ORGANISM       Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 540)
AUTHORS        Wilkie,T.M., Chen,Y., Gilbert,D.J., Moore,K.J., Yu,L., Simon,M.I.,
               Copeland,N.G. and Jenkins,N.A.
JL             Identification, chromosomal location, and genome organization of
               mammalian G-protein-coupled receptors
JOURNAL         Genomics 18 (2), 175-184 (1993)
MEDLINE        94116980
FEATURES       Location/Qualifiers
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BASE COUNT     90 a 173 c 137 g 140 t
ORIGIN

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Query Match 34.5%; Score 387; DB 10; Length 540;  
 Best Local Similarity 82.4%; Pred. No. 1.3e-57;

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QY 424 agcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 483
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Db 181 AGCCCTCTGGCCATCGCCATCGAGAGACAAGTGGCCCTCGCCAAAGGTCAAGCTCTACGGC 240
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Db 361 GTGCTGCCCTCTCTATGCTAAAGCGCTACGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 481 GATGTTGCTGCTCTCTCAGACGCTAGCCCTGCTCAAGAGCGGTCAACCATCGTACTGTTGGTGT 539

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Date: Dec 20, 2001 11:59 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -NATRIX=blosum62 -TRANS=human40.cdi
-1st=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-N=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEA_SIZE=500
-JEN=0 -MAXLEN=200000000 -USER=US09274752/@CENL1_8305
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-NO_XLPXY -WAIT -THREADS=1
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## Search information block:

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Query length: 353
Database: GenEmbl.*
Database sequences: 1472140
Database length: 341344837
Search time (sec): 2489.190000
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## score\_list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
gb_pr:AF034780	+ 1780.00	2355.68	4.5e-134	1062	AF034780 Homo sapiens lysosph
gb_pr:AC011511	+ 1767.00	2488.25	2.5e-130	156503	AC011511 Homo sapiens chrom
gb_hlg:AC073775	+ 1595.50	2238.11	2.2e-116	214006	AC073775 Mus musculus clone
gb_hlg:AC073781	+ 1589.50	2237.84	2.3e-116	220103	AC073781 Mus musculus clone
gb_ro:AF022138	+ 1589.50	2281.28	8.6e-119	1055	AF022138 Rattus norvegicus lys
gb_pat:AX085544	+ 1589.50	2281.25	8.6e-119	1059	AX085544 Sequence 7 from Paten
gb_pat:E07989	+ 1589.50	2280.54	9.4e-119	1139	E07989 DNA encoding a peptide
gb_ro:AB016931	+ 1589.50	2280.54	9.4e-119	1139	AB016931 Rattus norvegicus mRN
gb_pat:AR027718	+ 1589.50	2271.93	2.8e-118	2754	AR027718 Sequence 1 from Paten
gb_pat:132244	+ 1589.50	2271.93	2.8e-118	2754	132244 Sequence 1 from Paten
gb_ro:RNU10699	+ 1589.50	2271.93	2.8e-118	2754	RNU10699 Rattus norvegicus g-pro
gb_ro:AF108020	+ 1586.50	2276.93	1.5e-118	1059	AF108020 Mus musculus lysophos
g1 AF260256	+ 989.00	1415.64	1.4e-70	1110	AF260256 Danio rerio EDG-5-rel
gb_ro:AF090995	+ 898.00	1290.42	1.3e-63	607	AF090995 Cavia porcellus endothe
gb_ro:AF233365	+ 836.00	1194.87	2.8e-58	1149	AF233365 Homo sapiens G protei
gb_hlg:AL161741	+ 836.00	1153.77	5.5e-56	77678	AL161741 Homo sapiens chromos
gb_pr:HS057536	+ 836.00	1148.56	1.1e-55	132438	AL109741 Human DNA sequence
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gb_pat:132245	+ 826.00	1185.51	9.3e-58	2232	132245 Sequence 3 from Paten
gb_ro:AF108019	+ 826.00	1180.46	1.8e-57	1149	AF108019 Mus musculus lysophos
gb_pat:AX083645	+ 824.50	1159.76	7.0e-57	2757	AX083645 Sequence 10 from Paten
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gb_ro:AY011703	+ 809.50	1158.26	3.1e-56	978	AY011703 Castor canadensis EDG1
gb_ro:AY011726	+ 805.50	1152.51	6.4e-56	977	AY011726 Artibeus jamaicensis E
gb_ro:AY011708	+ 803.50	1149.62	9.3e-56	978	AY011708 Hystrix brachyurus EDG
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gb_ro:AY011715	+ 802.50	1148.18	1.1e-55	978	AY011715 Agouti taczanowski ED
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gb_ro:AY011711	+ 801.50	1146.01	1.5e-55	978	AY011711 Heterocephalus glaber
gb_ro:AY011694	+ 800.50	1145.29	1.6e-55	978	AY011694 Sorex araneus EDG1 (tl
gb_ro:AY011713	+ 800.50	1145.29	1.6e-55	978	AY011713 Hydrochaeris hydrochae
gb_ro:AY011690	+ 799.50	1143.85	1.9e-55	978	AY011690 Tamandua tetradactyla
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gb_om:AY011700 + 798.50 1142.41 2.3e-55 978 ! AY011700 Elephantulus ru
gb_om:AY011706 + 798.50 1142.41 2.3e-55 978 ! AY011706 Mus musculus ED
gb_ro:AF289990 + 798.00 1142.77 2.2e-55 876 ! AF289990 Cavia porcellus

seq_name: gb_pr:AF034780

seq_documentation_block:
LOCUS AF034780 1062 bp mRNA PRI 01-JAN-1999
DEFINITION Homo sapiens lysosphingolipid receptor Edg5 mRNA, complete cds.
ACCESSION AF034780
VERSION AF034780.1 GI:4090955
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1062)
AUTHORS MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.
TITLE Cloning and characterization of a putative G-protein coupled
receptor potentially involved in development
JOURNAL Mol. Cell. Neurosci. 5 (3), 201-209 (1994)
MEDLINE 94373324
REFERENCE 2 (bases 1 to 1062)
AUTHORS An,S.
TITLE Edg5, a Human homolog of rat H218 that is a functional receptor for
lysosphingolipids
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1062)
AUTHORS An,S.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
Ave., San Francisco, CA 94143-0711, USA
FEATURES
Location/Qualifiers
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CAIVENLLVLIAYARKSKFHSAMYLFLGNLAADLLAGVAFVANTLLSGVTLRLTP
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VLGGLPILGNLCILGHACSTVLPYAKHVLCVVTFTSIILLAIVLYRVYCVRS
SHADMAAPOTLALKTKTIVLGVFVCLWLPASFILLDYACPVHSCPLYKAHFFAV
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BASE COUNT 166 a 367 c 294 g 235 t  
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Quality: 1780.00 Length: 353  
Ratio: 5.086 Gaps: 0  
Percent Similarity: 99.150 Percent Identity: 99.150

## alignment\_block:

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17 styAsnTyrThrLysGluThrLeuGluThrGlnGluThrSerArg 34
51 CTATATTATACCAAGGACGCGTGAACGAGGAGGACGACCTCCGCC 100
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101  ACGTGGCCTCGGCCTTCATCGTCATCCTCTGTGGCCCAATGTGGTGAA 150
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51  AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
|||||
151  AACCTTCTGTGCTCATTTGGGTGGCCGGAACAGCAAGTTCACCTGGC 200
|||||
67  MetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuAlaGlyV 84
|||||
201  AATGTACCTTGTCTGGGAACCTGGCCGCTCCGATCTACTGCGAGCG 250
|||||
84  AlaAlaPheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
|||||
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|||||
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|||||
301  ACGCCTGTGCAGTGGTTTGGCCGGAGGCTCTGCCTCCATCAGCTCTC 350
|||||
117  rAlaSerValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaI 134
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351  GGCTCTGTCTTACGCTCTCGGCCATCGCCATGTAGCGCCACGTGCCA 400
|||||
34  leAlaLysValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeu 150
|||||
401  TTGCCAAGGTCAAGCTGTATGGCAGCACAAGAGCTGCCGCATGCTTCG 450
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151  LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProIl 167
|||||
451  CTATCGGGGCCCTCGTGGCTCATCTCGTGGCTCGTGGTGGCTGCCAT 500
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167  eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuP 184
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501  CCTGTGCTGGAATGCTGTGGCCACCTCGAGGCTGTCTCCACATGCTCT 550
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184  roLeuTyrAlaLysHisTyrValLeuCysValValThrIlePheSerIle 200
|||||
551  CTCTCTACGCCAAGCATATTGCTGTGCTGTGGTGTGACCATCTCTCCAT 600
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201  IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValValAr 217
|||||
601  ATCCTCTGTGCCATCGTGGCCCTGTACGTGCGCATCTACTGCGTGTCCG 650
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217  gSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLeuLys 234
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701  CGGTACCATCGTGTAGGCTCTTATCGTCTGCTGGCTGCCGCTTC 750
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267  uTyrLysAlaHisTyrPhePheAlaValSerThrLeuAsnSerLeuLeu 284
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851  ACCCGCTCATCTACAGTGGCGGAGCGCGGACCTGCGCGGGAGTGTCTT 900
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301  ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArg 317
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901  CGGCCGCTGCAGTGTCTGGCGCGGGGGTGGGGTGCAGGACGAGGCG 950
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DEFINITION Homo sapiens chromosome 19 clone CTD-2369p2, complete sequence.
ACCESSION AC011511
VERSION AC011511.10 GI:15187226
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Unpublished
2 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Aug 15, 2001 this sequence version replaced gi:14971180.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
STS Content:
WI-14289 G22683
WI-7031 G06361.
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BASE COUNT 35365 a 41856 c 41375 g 37907 t
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Quality: 1767.00 Length: 353  
Ratio: 5.078 Gaps: 0  
Percent Similarity: 98.584 Percent Identity: 98.584

## alignment\_block:

US-09-274-752D-3 x AC011511

Align seg 1/1 to: AC011511 from: 1 to: 156503

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17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArg 34
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34 InValAlaSerAlaGlyIleValIleLeuCysCysAlaIleValValGlu 50
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51 AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
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117106 AACCTCTGGTGCATATTGGCGGTGGCGGAGCAAGCAAGTTCACCTCGGC 117155
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67 aMetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGlyV 84
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117156 AATGTACCTGTTCTGGGCAACCTGGCGCTCCGATCTACTGGCAGCG 117205
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84 alAlaPheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
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117206 TGGCCTTCGTAGCAATACCTGTCTCTGGCTCTGTCAAGCTGAGGCTG 117255
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101 ThrProValGlnTyrPheAlaArgGluGlySerAlaSerIleThrLeuSe 117
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456 ACGCCTGTGAGTGGTTGGCGGAGGGCTGTGCCTTCATCACCTCTC 117305
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117 rAlaSerValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaI 134
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151 LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProIl 167
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167 eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuP 184
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117656 CGGTACCATCGTGTAGCGCTCTTATCGTCTGCTGGCTGCGCCGCTTC 117705
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DEFINITION Mus musculus clone RP23-382B11, WORKING DRAFT SEQUENCE, 9 ordered
pieces.
ACCESSION AC073775
VERSION AC073775.2 GI:9256790
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE house mouse
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 214006)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810392.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1883595
Center clone name: RPCI-23_382B11
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Summary Statistics
Consensus quality: 209197 bases at least Q40
Consensus quality: 212478 bases at least Q30
Consensus quality: 212996 bases at least Q20
Estimated insert size: 218930; agarose-fp estimation
Estimated insert size: 213656; sum-of-contigs estimation
Quality coverage: 9.1 in Q20 bases; agarose-fp estimation
Quality coverage: 9.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 11489: contig of 11489 bp in length
* 11490 11589: gap of unknown length
* 11590 72347: contig of 60758 bp in length
* 72348 72447: gap of unknown length
* 72448 79269: contig of 6822 bp in length
* 79270 79369: gap of unknown length
* 79370 79945: contig of 576 bp in length
* 79946 80046: gap of unknown length
* 80046 101339: contig of 21294 bp in length
* 101340 101439: gap of unknown length
* 101440 118105: contig of 16666 bp in length
* 118106 118205: gap of unknown length
* 118206 142604: contig of 24399 bp in length
* 142605 142704: gap of unknown length
* 142705 151311: contig of 8607 bp in length
* 151312 151411: gap of unknown length
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Location/Qualifiers
FEATURES
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 ORIGIN

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 Ratio: 4.734 Gaps: 1  
 Percent Similarity: 95.467 Percent Identity: 89.235

alignment\_block:

US-09-274-752D-3 x AC073775

Align seg 1/1 to: AC073775 from: 1 to: 214006

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17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArg 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
J49 CTACAATTACACCAAGAGAGAGCTGGACATGCAGGAGACCACTCCCGCA 14098
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34 InValAlaSerAlaGlyLeuValLeuLysCysAlaLeuValValGlu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14099 AGGTGGCTGGCTTCATCATCATATCTGTCTGGCCATCGTGGTGGA 14148
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14149 AATCTTCTGGTGCTCATTCAGAGTGGCCAGGACAGCAAGATTCACCTCAGC 14198
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14199 AATGACCTGTCTTGGCAACCTGGCAGCTCTGACCTGTGGCAGGCG 14248
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84 alaAlaPheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
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201 IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValValAr 217
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217 gSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLeuLysT 234
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seq_name: gb_htg.AC073781
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LOCUS AC073781 220103 bp DNA HTG 02-SEP-2000
DEFINITION Mus musculus clone RP23-398A12, WORKING DRAFT SEQUENCE, 13 ordered
pieces.
ACCESSION AC073781
VERSION AC073781.2 GI:9964815
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 220103)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
2 (bases 1 to 220103)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 2, 2000 this sequence version replaced gi:8810398.
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1889716
Center clone name: RPCI-23_398A12
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Summary Statistics
Consensus quality: 209550 bases at least Q40
Consensus quality: 216439 bases at least Q30
Consensus quality: 217881 bases at least Q20
Estimated insert size: 22880; agarose-fp estimation
Estimated insert size: 21953; sum-of-contigs estimation
Quality coverage: 6.87 in Q20 bases; agarose-fp estimation

```

Quality coverage: 6.98 in Q20 bases; sum-of-contigs estimation.

\* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

- \* 40803: contig of 40803 bp in length
- \* 40804: gap of unknown length
- \* 40904: contig of 620 bp in length
- \* 41524: gap of unknown length
- \* 41624: contig of 14088 bp in length
- \* 55712: gap of unknown length
- \* 55812: contig of 6001 bp in length
- \* 61813: gap of unknown length
- \* 61912: contig of 55694 bp in length
- \* 117607: gap of unknown length
- \* 117707: contig of 4567 bp in length
- \* 122274: gap of unknown length
- \* 122374: contig of 1029 bp in length
- \* 123403: gap of unknown length
- \* 123503: contig of 1291 bp in length
- \* 124794: gap of unknown length
- \* 124894: contig of 3072 bp in length
- \* 127966: gap of unknown length
- \* 128066: contig of 22714 bp in length
- \* 150780: gap of unknown length
- \* 150880: contig of 19773 bp in length
- \* 170653: gap of unknown length
- \* 170753: contig of 42763 bp in length
- \* 213516: gap of unknown length
- \* 213616: contig of 6488 bp in length.

FEATURES.

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/clone="RP23-398A12"  
/clone\_lib="RPCI mouse BAC library 23"  
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a ment\_scores:  
Quality: 1595.50 Length: 353  
Ratio: 4.734 Gaps: 1  
Percent Similarity: 95.467 Percent Identity: 89.235

alignment\_block:

US-09-274-752D-3 x AC073781

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- 17 tTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArgC 34
- 173364 CTACAATTACCAAGGACGCTGGACATGTCAGGAGACCACTCCCGCA 173413
- 34 InValAlaSerAlaGlyIleValIleLeuCysCysAlaIleValValGlu 50
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- 51 AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
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DEFINITION   Rattus norvegicus lysophospholipid receptor (h218) mRNA, partial cds.
ACCESSION   AF022138
VERSION     AF022138.1   GI:2668609
KEYWORDS    Norway rat.
SOURCE      Rattus norvegicus
ORGANISM    Rattus norvegicus
REFERENCE   1 (bases 1 to 1056)
AUTHORS     MacLennan,A.J., Brose,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.
TITLE       Cloning and characterization of a putative G-protein coupled receptor potentially involved in development
JOURNAL     Mol. Cell. Neurosci. 5 (3), 201-209 (1994)
MEDLINE     94373324
REFERENCE   2 (bases 1 to 1056)
AUTHORS     An,S., Bleu,T., Huang,W., Hallmark,O.G., Coughlin,S.R. and Goetzl,E.J.
TITLE       Identification of cDNAs encoding two G protein-coupled receptors for lysophospholipids
JOURNAL     FEBS Lett. 417 (3), 279-282 (1997)
REMARKS     98072391
REMARKS     3 (bases 1 to 1056)
AUTHORS     An,S.
TITLE       Direct Submission
JOURNAL     Submitted (02-SEP-1997) Medicine, UCSF, San Francisco, CA
JOURNAL     94143-0711, USA
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67  aMetTyLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGlyV 84
201  CATGTACTGTTCCTCGCAACCTGGCAGCCTCGGACCTGTGGCAGCG 250
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251  TGGCTTCGTGGCAACACACTTGTCTCCGACCTGTCCACCTGTCCTTA 300
101  ThrProValGlnTrpPheAlaArgGluGlySerAlaSerIleThrLeuSe 117
301  ACTCCCTTGGAGTGGTTTGGCCGAGAGGTTTCAGCCTTCATCAGCTCTC 350
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251  SerIleLeuLeuLeuAspTyTrpAlaCysProValHisSerCysProIle 267
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334  euGluArgGlyMetHisMetProThrSerProThrPheLeuGluGlyAsn 350

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DEFINITION DNA encoding a peptide that has receptor activity coupling with
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ACCESSION E07989
VERSION E07989.1 GI:2176120
KEYWORDS JP 1994234797-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1139)
AUTHORS Takuwa,A.
TITLE NEW PEPTIDE HAVING RECEPTOR ACTIVITY AND DNA ENCODING THE PEPTIDE
JOURNAL Patent: JP 1994234797-A 1 23-AUG-1994;
COMMENT TSUMURA & CO, TAKUWA AKIRA
OS Homo sapiens (human)
PN JP 1994234797-A/1
PD 23-AUG-1994
PF 10-FEB-1993 JP 1993044330
PI TAKUWA AKIRA
PC C07K13/00,C07H21/04,C12N15/12,C12P21/02;
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CC topology: Linear;
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ACCESSION AB016931
VERSION AB016931.1 GI:3445557
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Rattus.
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AUTHORS       Gonda,K. and Takuwa,Y.
TITLE         Direct Submission
JOURNAL       Submitted (13-AUG-1998) to the DDBJ/EMBL/GenBank databases. Koichi
Gonda, University of Tokyo, Molecular and Cellular Physiology;
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail:gonda@em.u-tokyo.ac.jp, Tel:81-3-3812-2111,
Fax:81-3-5800-6845)
REFERENCE     2 (sites)
AUTHORS       Okazaki,H., Ishizaka,N., Sakurai,T., Kurokawa,K., Goto,K.,
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TITLE         Molecular cloning of a novel putative G protein-coupled receptor
expressed in the cardiovascular system
JOURNAL       Biochem. Biophys. Res. Commun. 190 (3), 1104-1109 (1993)
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 ORGANISM Unknown.  
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 AUTHORS MacLennan, A. John.  
 TITLE Molecular cloning and expression of G-protein coupled receptors  
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 AUTHORS MacLennan, A. J.  
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 JOURNAL Patent: US 5585476-A 1 17-DEC-1996;  
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Rattus.

REFERENCE 1 (bases 1 to 2754)  
MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.

AUTHORS Cloning and characterization of a putative G-protein coupled  
TITLE receptor potentially involved in development

JOURNAL Mol. Cell. Neurosci. 5, 201-209 (1994)  
MEDLINE 94373324

REFERENCE 2 (bases 112 to 1250)  
Okazaki,H., Ishizaka,N., Sakurai,T., Kurokawa,K., Goto,K.,

AUTHORS Kumada,M. and Takuwa,Y.  
TITLE Molecular cloning of a novel putative G protein coupled receptor

JOURNAL Biochem. Biophys. Res. Commun. 190, 1104-1109 (1993)  
MEDLINE 93176155

REFERENCE 3 (bases 1 to 2754)  
MacLennan,A.J.

AUTHORS Direct Submission  
TITLE Submitted (14-JUN-1994) MacLennan A. J., University of Florida,

JOURNAL Neuroscience, 1600 S.W. Archer Road, Gainesville, FL 32610, USA  
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17 STYrAsnTyrThrLysGluThrLeuGluThrGlnGluThrSerArgG 34
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117 rAlaSerValGlySerLeuAlaIleAlaIleGluArgHisValAlaI 134
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DEFINITION Mus musculus lysophospholipid receptor B2 (lpb2) gene, complete cds.
ACCESSION AF108020
VERSION AF108020.1 GI:4324650
KEYWORDS house mouse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
REFERENCE 1 (bases 1 to 1059)
AUTHORS Zhang, G., Contos, J.J., Weiner, J.A., Fukushima, N. and Chun, J.
TITLE Comparative analysis of three murine G-protein coupled receptors
activated by sphingosine-1-phosphate
JOURNAL Gene 227 (1), 89-99 (1999)
MEDLINE 99132320
REFERENCE 2 (bases 1 to 1059)
AUTHORS Zhang, G., Contos, J.J.A. and Chun, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1998) Pharmacology, School of Medicine,
University of California at San Diego, 9500 Gilman Drive, La Jolla,
CA 92093-0636, USA
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LOCUS AF260256 1110 bp mRNA VRT 27-JUL-2000
DEFINITION Danio rerio EDG-5-related protein mRNA, partial cds.
ACCESSION AF260256
VERSION AF260256.1 GI:9502146
KEYWORDS zebrafish.
SOURCE
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE
AUTHORS Kupperman,E., An,S., Osborne,N., Waldron,S. and Stainier,D.Y.
TITLE A sphingosine-1-phosphate receptor regulates cell migration during
vertebrate heart development
JOURNAL Nature 406 (6792), 192-195 (2000)
MEDLINE 20365730
REFERENCE
AUTHORS Kupperman,E., An,S., Osborne,N., Waldron,S. and Stainier,D.Y.R.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2000) Biochemistry, UCSF, 513 Parnassus Ave, San
Francisco, CA 94143, USA
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ACCESSION      AF289992
VERSION        AF289992.1 GI:15077230
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ORGANISM      Cavia porcellus
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REFERENCE      1 (bases 1 to 607)
AUTHORS        Segura,B.J., Xiao,L., Cowles,R.A., Turner,D.J., Logsd
                Mulholland,M.W.
TITLE          Sphingosine-1-phosphate Mediates Calcium Signaling i
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 607)
AUTHORS        Xiao,L. and Mulholland,M.W.
TITLE          Direct Submission
JOURNAL        Submitted (26-JUL-2000) Surgery, University of Michi
                Medical Center Drive, Ann Arbor, MI 48109-0331, USA
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US-09-274-752D-3 x AF289992

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 53 euValLeuIleAlaValAlaArgAsnSerLysPheHisSerAlaMetTyr 69  
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 DEFINITION Rattus norvegicus putative G-protein coupled receptor (GPCR18)  
 mRNA, partial cds.

ACCESSION AF090995

VERSION AF090995.1 GI:10880457

KEYWORDS

SOURCE

ORGANISM

Norway rat.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 573)

AUTHORS Carroll, S.L., Miller, M.L. and Benedict-Hamilton, H.M.

TITLE Identification and characterization of novel G-protein coupled

receptors expressed in regenerating peripheral nerve  
 Unpublished

JOURNAL 2 (bases 1 to 573)

AUTHORS Carroll, S.L., Miller, M.L. and Benedict-Hamilton, H.M.

TITLE Direct Submission

JOURNAL Submitted (11-SEP-1998) Pathology, University of Alabama at  
 Birmingham, LHRB513, 701 South 19th Street, Birmingham, AL  
 35294-0007, USA

FEATURES Location/Qualifiers

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US-09-274-752D-3 x AF090995

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102 CCATCGAGAGACAAGTGGCCATCCCAAGGTCAAGCTCTACGGCAGTGC 151

144 LysSerCysArgMetLeuLeuLeuIleGlyAlaSerTrpLeuIleSerLe 160

152 AAAAGCTGTCAATGTTGATGCTCATTTGGGGCCCTCTTGGCTGATATCGCT 201

160 uValLeuGlyGlyLeuProIleLeuGlyTrpAsnCysLeuGlyHisLeuG 177

202 GATTCTGGTGGCTTGGCCATCTCTGGCTGGAATGCTGGACCATCTGG 251

177 luAlaCysSerThrValLeuProLeuTyrAlaLysHisTyrValLeuCys 193

252 AGGCTTGCTCCACTGTGCTGCCCTCTATGCTAAGCCTATGTGCTCTGC 301

194 ValValThrIlePheSerIleIleLeuLeuAlaIleValAlaLeuTyrVa 210

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227 lThrLeuAlaLeuLeuLysThrValThrIleValLeuGlyValPheIle 243

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244 ValCysTrpLeuProAlaPheSerIleLeuLeuLeuAspTyrAlaCysPr 260
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260 oValHisSerCysProIleLeuTyrLysAlaHisTyrPhePheAlaVals 277
   ||:::|
502 CGTCGGGGCTGCTCCTGTCCCTACAAAGCCCATTTCTTTGGCCTTCG 551
277 erThrLeuAsnSerLeuLeu 283
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552 CCACCCCTCAACTCTCTGCTC 571
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score_list:	Strtd Orig	zScore	EScore	Len	Documentation
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gb.pat:AF011466	+ 1365.00 2898.89	3.4e-153	1734	!	AF011466 Homo sapiens G-protein
gb.pr:AF233092	+ 1952.00 2883.47	2.5e-152	1159	!	AF233092 Homo sapiens lysophos
gb.pr:AF197929	+ 1946.00 2870.32	1.3e-151	1810	!	AF197929 Homo sapiens short fo
gb.pr:AB060872	+ 1918.00 2827.33	3.3e-149	2115	!	AB060872 Macaca fascicularis H
gb.pr:AC002306	+ 1899.50 2312.68	1.5e-120	38651	!	AC002306 Homo sapiens DNA fro
gb.htg:AC011458	+ 1589.50 2303.10	5.2e-120	105412	!	AC011458 Homo sapiens chromo
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gb.htg:AC073687	+ 1317.50 1893.77	3.3e-97	201331	!	AC073687 Mus musculus clone
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gb.ov:XA249844	+ 962.50 1411.95	2.3e-70	1941	!	XA249844 Xenopus laevis mRNA f
gb.ov:XA249843	+ 962.50 1411.41	2.4e-70	2053	!	XA249843 Xenopus laevis mRNA f
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gb.pr:MMU070622	+ 960.00 1406.83	4.4e-70	2250	!	MMU070622 Mus musculus lysophosph
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gb.pr:AF014418	+ 959.50 1409.69	3.0e-70	1543	!	AF014418 Rattus norvegicus end
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gb.pr:HSXED2	+ 956.00 1406.77	4.4e-70	1217	!	HSXED2 Homo sapiens mRNA for G p
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gb.pr:MMU48235	+ 953.50 1401.49	8.7e-70	1436	!	MMU48235 Mus musculus putative G
gb.om:U18405	+ 948.00 1392.12	2.9e-69	1631	!	U18405 Ovis aries putative G-H
gb.om:BTU48236	+ 942.00 1383.70	8.5e-69	1256	!	BTU48236 Bos taurus putative G-H
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gb.pr:AF186380	+ 857.50 1262.08	5.1e-62	1062	!	AF186380 Homo sapiens calcium-
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gb.htg:AL590646	+ 752.50 1054.18	1.9e-50	252828	!	AL590646 Homo sapiens chromo
gb.pr:HMOLUP44	+ 731.00 1036.20	8.8e-53	2462	!	HMOLUP44 Mus musculus lysophos
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117 aSerValAlaThrLeuLeuAlaIleAlaValGluArgHisArgSerValM 134
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435 GTCGGTGGCCACACTGCTGGCCATCGCTGGAGCGGCACCGAGTGA 484
134 eAlaValGlnLeuHisSerArgLeuProArgGlyArgValValMetLeu 150
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485 TGCCGCTGAGCTGACACACCGCTGCCCCGCGGCGGTCATGTC 534
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167 sSerTrpHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
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635 TGCTCAGCCGCTCTATTTGGCGCTGGGCTGTGTCGAGCGCTTGTG 684
201 PheLeuLeuMetValAlaValTyrThrArgIlePhePheTyrValArgAr 217
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685 TTCCTGCTCATGCTGGCTGTGTACACCGCATTTCTTCTACGTGGCGG 734
217 gArgValGlnArgMetAlaGluHisValSerCysHisProArgTyrArgG 234
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735 GCGAGTGCAGCATGGCAGAGCATGTCAGTGCACACCCCGCTACCGAG 784
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935 CCGAGCGCAACTCAGTGGTCAATGCTGCTGTGCTTCTTGGCGAGATGCT 984
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seq\_name: gb\_pr:AF233092

seq\_documentation\_block: 1159 bp mRNA PRI 17-AUG-2000

LOCUS AF233092 Homo sapiens lysophosphatidic acid G protein-coupled receptor 4

DEFINITION Homo sapiens lysophosphatidic acid G protein-coupled receptor 4 (EDG4) mRNA, complete cds.

ACCESSION AF233092

VERSION AF233092.1 GI:7243675

KEYWORDS

SOURCE human;

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1159) Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K. Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K. Lysophosphatidic acid (LPA) receptors of the EDG family are differentially activated by LPA species. Structure-activity relationship of cloned LPA receptors

TITLE PEBS Lett. 478 (1-2), 159-165 (2000)

JOURNAL MEDLINE 20382744

REFERENCE 2 (bases 1 to 1159) Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K. Direct Submission

AUTHORS Submitted (09-FEB-2000) Graduate School of Pharmaceutical Sciences, The University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

FEATURES

source Location/Qualifiers

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/db\_xref="taxon:9606"

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Ratio: 5.110 Gaps: 1

Percent Similarity: 99.739 Percent Identity: 99.478

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seq\_name: gb\_pr:AF197929

seq\_documentation\_block:

LOCUS AF197929 1810 bp mRNA PRI 01-NOV-2000  
DEFINITION Homo sapiens short form lysophosphatidic acid receptor EDG4 (EDG4)  
mrna, complete cds.

ACCESSION AF197929  
VERSION AF197929.1 GI:11066253

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1810)

AUTHORS An.S., Bleu.T., Hallmark.O.G. and Goetzl.E.J.

TITLE Characterization of a novel subtype of human G protein-coupled  
receptor for lysophosphatidic acid

JOURNAL J. Biol. Chem. 273 (14), 7906-7910 (1998)

MEDLINE 98192573

PUBMED 9525886

REFERENCE 2 (bases 1 to 1810)

AUTHORS An.S.

TITLE Human Edg4 lysophosphatidic acid receptor cDNA encoding a putative  
protein with COOH-terminus different from the previously-reported  
Edg4

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1810)

AUTHORS An.S.

TITLE Direct Submission

Submitted (22-OCT-1999), Medicine, UCSF, 533 Parnassus, Room Ub-8,  
San Francisco, CA 94143-0711, USA

JOURNAL Location/Qualifiers

FEATURES

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BASE COUNT 348 a 561 c 514 g 387 t

ORIGIN

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Ratio: 5.108

Percent Similarity: 99.478

Percent Identity: 99.217

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Length: 383

Gaps: 1

Align seg 1/1 to: AF197929 from: 1 to: 1810 GFFV

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169 TAACAACAGTGGCAAGAGCTCAGCTCCACCTGGCGGCCCAAGGATGG 218
34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
219 TCGTGGTGGCACTGGGGCTGACCGTCAAGCTGCTGGTGGTGGTGGTGG 268
51 LeuLeuValIleAlaAlaIleAlaSerAsnArgArgPheHisGlnProII 67
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67 eTyrTyrLeuLeuGlyAsnLeuAlaAlaAlaAspLeuPheAlaGlyValA 84
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101 LeuGluGlyTyrPheLeuArgGlnGlyLeuLeuAspThrSerLeuThrAl 117
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1169 CTTTAGTACTTGAACCTTCAGCGTACGCGGCAAGCAACAATCCACAG 1218
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seq\_documentation\_block:

LOCUS AB060872 2115 bp mRNA PRI 13-JUN-2001  
DEFINITION Macaca fascicularis brain cDNA clone:Qtra-12246, full insert sequence.

ACCESSION AB060872

VERSION AB060872.1 GI:13874529

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Macaca fascicularis adult male temporal lobe right cDNA to mRNA, clone\_lib:macaque brain cDNA library Qtra clone:Qtra-12246.

ORGANISM

Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.

REFERENCE

AUTHORS Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.

TITLE Isolation of full-length cDNA clones from macaque brain cDNA libraries

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2115)

AUTHORS Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama

1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)

Lab host: TOP10

Vector: pME18S-FL3 (Acc.No. AB009864)

R. Site1: DraIII (CAGCTGTG)

R. Site2: DraIII (CAGCTGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer

[ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method

(Sugano et al., Institute of Medical Science, University of Tokyo).

Custom primer used for sequencing

{ 5' end primer [CTTCTGCTCTAAAGCTGCG];

3' end primer [CGACCTGCAGCTCGAGCACA] }.

Location/Qualifiers

1. .2115

/organism="Macaca fascicularis"

/db\_xref="taxon:9541"

/clone="Qtra-12246"

FEATURES

source

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ORIGIN

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Quality: 1918.00 Length: 383
Ratio: 5.034 Gaps: 1
1 .nt Similarity: 99.478 Percent Identity: 97.650

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US-09-274-752D-1 x AB060872

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Align seg 1/1 to: AB060872 from: 1 to: 2115

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234 luThrThrLeuSerLeuValTyrThrValValIleIleLeuGlyAlaPhe 250
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251 ValValCysTrpThrProGlyGlnValValLeuLeuLeuAspGlyLeuGl 267
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seq_documentation_block:

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DEFINITION Homo sapiens DNA from chromosome 19-cosmid R3799, genomic
sequence, complete sequence.
ACCESSION AC002306
VERSION AC002306.1 GI:2213634
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 38651)

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AUTHORS
Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Danganan,L., Bruce,R., Ramirez,M., Stillwagen,S., Garnes,J.,
Olsen,A.O. and Carrano,A.V.

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TITLE
anonymous cosmid from 19p12

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JOURNAL
Unpublished (1997)

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REFERENCE
2 (bases 1 to 38651)
Lamerdin,J.E.

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AUTHORS
Direct Submission

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TITLE
Submitted (24-JUN-1997) Human Genome Center, Lawrence Livermore

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JOURNAL

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seq\_name: gb\_htg:AC011458

seq\_documentation\_block:  
LOCUS AC011458 105412 bp DNA HTG 26-JUL-2001  
DEFINITION Homo sapiens chromosome 19 clone CTC-412M14, \*\*\* SEQUENCING IN  
PROGRESS \*\*\*, 2 ordered pieces.

ACCESSION AC011458  
VERSION AC011458.6 GI:15022005  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_ACTIVEFIN.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 105412)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 105412)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 26, 2001 this sequence version replaced gi:9256295.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 67802: contig of 67802 bp in length  
\* 67803 67902: gap of unknown length  
\* 67903 105412: contig of 37510 bp in length.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
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Project Information  
Center Project Name: 343690  
Center clone name: CTC-412M14  
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Summary Statistics  
Consensus quality: 104543 bases at least Q40  
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Consensus quality: 104736 bases at least Q20  
Estimated insert size: 107130; agarose-fp estimation  
Estimated insert size: 104798; sum-of-contigs

estimation  
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estimation  
estimation.  
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1. .105412  
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BASE COUNT 26159 a 25740 c 26109 g 27304 t 100 others  
ORIGIN

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Quality: 1589.50 Length: 1041  
Ratio: 4.161 Gaps: 3  
Percent Similarity: 36.695 Percent Identity: 36.503

alignment\_block:  
US-09-274-752D-1 x AC011458/rev

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DEFINITION Sequence 3 from patent US 5998164.
ACCESSION AR092424
VERSION AR092424.1 GI:10019178
KEYWORDS
SOURCE
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REFERENCE 1 (bases 1 to 2185)
IORS Li,Y., Cao,L., Ni,J., Gentz,R., Bult,C.J., Sutton,G.G. III and
Rosen,C.A.
TITLE Polynucleotides encoding human G-protein coupled receptor GPR2
JOURNAL Patent: US 5998164-A 3 07-DEC-1999;
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alignment_block:
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seq_name: gb_htg:AC073687

seq_documentation_block:
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1 JITION Mus musculus clone RP23-138B15, WORKING DRAFT SEQUENCE, 36
unordered pieces.
ACCESSION AC073687
VERSION AC073687.1 GI:8810304
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1789903
Center clone name: RPCI-23_138B15
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Summary Statistics
Consensus quality: 170890 bases at least Q40
Consensus quality: 185810 bases at least Q30
Consensus quality: 188737 bases at least Q20
Estimated insert size: 207000; agarose-fp estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.17 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1008 1107: gap of unknown length
1108 2256: contig of 1149 bp in length
2257 2356: gap of unknown length
2357 3666: contig of 1310 bp in length
3667 3766: gap of unknown length
3767 5071: contig of 1305 bp in length
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Percent Similarity: 33.771 Percent Identity: 31.051

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US-09-274-752D-1 x AC073687/rev

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DEFINITION Xenopus laevis mRNA for lysophosphatidic acid receptor (lpalr
gene), clone 10.
ACCESSION AJ249844
VERSION AJ249844.1 GI:6523553
KEYWORDS lpalr gene; lysophosphatidic acid receptor.
SOURCE African clawed frog.
ORGANISM
Xenopus laevis
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 1941)
Kimura,Y., Schmitt,A., Fukushima,N., Ishii,I., Kimura,H.,
Nebreda,A.R. and Chun,J.
Two Novel Xenopus Homologs of Mammalian LPAL/EDG-2 Function as
Lysophosphatidic Acid Receptors in Xenopus Oocytes and Mammalian
Cells
J. Biol. Chem. 276 (18), 15208-15215 (2001)
11278944
REFERENCE 2 (bases 1 to 1941)
Nebreda,A.R.
Direct Submission
Submitted (29-SEP-1999) Nebreda A.R., Developmental Biology
Programme, EMBL, Meyerhofstrasse 1, 69117 Heidelberg, GERMANY
JOURNAL
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DEFINITION Xenopus laevis mRNA for lysophosphatidic acid receptor (lpalr
gene), clone 1.
ACCESSION AJ249843
VERSION AJ249843.1 GI:6523551
KEYWORDS lpalr gene; lysophosphatidic acid receptor.
SOURCE African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 2053)
Kimura,Y., Schmitt,A., Fukushima,N., Ishii,I., Kimura,H.,
Nebreda,A.R. and Chun,J.
Two Novel Xenopus Homologs of Mammalian lPA1/EDG-2 Function as
Lysophosphatidic Acid Receptors in Xenopus Oocytes and Mammalian
Cells
J. Biol. Chem. 276 (18), 15208-15215 (2001)
JOURNAL
11278944
PUBMED
2 (bases 1 to 2053)
REFERENCE
Nebreda,A.R.
AUTHORS
Direct Submission
TITLE
Submitted (29-SEP-1999) Nebreda A.R., Developmental Biology
Programme, EMBL, Meyerhofstrasse 1, 69117 Heidelberg, GERMANY
JOURNAL
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ACCESSION AR116996
VERSION AR116996.1 GI:14097902
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REFERENCE
1 (bases 1 to 2250)
AUTHORS Chun,J.J.M. and Hecht,J.H.
TITLE Cloned lysophosphatidic acid receptors
JOURNAL Patent: US 6140060-A 1 31-OCT-2000;
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ACCESSION U70622

VERSION U70622.1 GI:1655990

KEYWORDS lysophosphatidic acid receptor; G-protein coupled receptor.

SOURCE house mouse.

ORGANISM Mus musculus

RENCHE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS Hecht, J.H., Weiner, J.A., Post, S.R. and Chun, J.

TITLE Ventricular zone gene-1 (vzg-1) encodes a lysophosphatidic acid receptor expressed in neurogenic regions of the developing cerebral cortex

JOURNAL J. Cell Biol. 135 (4), 1071-1083 (1996)

MEDLINE 97081105

REFERENCE 2 (bases 1 to 2250)

AUTHORS Hecht, J.H., Weiner, J.A., Post, S.R. and Chun, J.

TITLE Direct submission

JOURNAL Submitted (12-SEP-1996) Pharmacology, University of California at

San Diego, School of Medicine, 9500 Gilman Drive, La Jolla, CA

92093-0636, USA

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US-09-274-752D-1 x MMU70622

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39 lyLeuThrValSerValLeuValLeuLeuLeuThrAsnLeuValIleAla 55

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56 AlaIleAlaSerAsnArgPheHisGlnProIleTyrTyrLeuLeuGl 72

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122 uLeuAlaIleAlaValGluArgHisArgSerValMetAlaValGlnLeuH 139

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156 ValAlaAlaLeuGlyLeuGlyLeuLeuProAlaHisSerTrpHisCysLe 172

744 ACTATGGCCATGTGATGGGTGCTATACCCAGTGGGCTGGGAACGTGAT 793

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794 CTGTGATATCGATCTGTTCCACATGGCACCCCTCTACAGTACTCTCT 843

189 yLeuAlaValTrpAlaLeuSerSerLeuValPheLeuLeuMetVal 205

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ACCESSION A87639
VERSION A87639.1 GI:6736276
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 1543)
Schwartz,J. and Allard,J.
THORS
TITLE DIAGNOSTIC AND THERAPEUTIC USE OF A POLYPEPTIDE WITH OB25 RECEPTOR
ACTIVITY EXPRESSED BY MYELIN PRODUCING CELLS
JOURNAL Patent: WO 9836060-A 1 20-AUG-1998:
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR)
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US-09-274-752D-1 x A87639

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2001, 09:15:21 ; Search time 2907.25 Seconds  
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9839.577 Million cell updates/sec

Title: US-09-274-752D-2

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Gapop 10.0 , Gapext 1.0

Summary: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.om.\*
- 20: em.or.\*
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- 30: em.htgo\_hum.\*
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- 32: em.htgo\_rnd.\*
- 33: em.htg\_rnd.\*
- 34: em.htg\_inv.\*
- 35: em.htg\_rnd.\*
- 36: em.htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1140.6	65.8	1159	9	AF233092	Homo sapi
6	885.2	51.0	38651	9	AC002306	Homo sapi
7	883.6	51.0	105412	2	AC011458	Homo sapi
8	860.4	49.6	2185	2	AR092424	Sequence
9	594	34.3	201331	2	AC073687	Mus muscu
10	572.6	33.0	5618	10	AF218844	Mus muscu
11	365.6	21.1	1543	6	AB7639	Sequence 1
12	365.6	21.1	1543	10	AF014418	Rattus no
13	364	21.0	2250	6	AR116996	Sequence
14	364	21.0	2250	10	MMU70622	Mus muscu
15	362.4	20.9	1436	10	MMU48235	Mus muscu
16	362.4	20.9	2170	10	AF090347	Rattus no
17	342.4	19.7	1552	4	BTU48236	Bos tauru
18	341.8	19.7	1631	4	U18405	Ovis arie
19	329	19.0	1576	9	HSU80811	Human lysop
20	327.4	18.9	2687	9	AK022808	Homo sapi
21	325.8	18.8	1110	6	AX085538	Sequence
22	325.8	18.8	1217	9	HSEDG2	Sequence
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36	264	15.2	2374	10	AF097733	Rattus no
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38	256.6	14.8	90500	2	AL603785	Danio rer
39	213.8	12.3	5557	10	AF272364S1	Mus muscu
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41	213.8	12.3	110000	2	AC068947_3	Continuation (4 of
42	213	12.3	133747	9	AL139150	Human DNA
43	213	12.3	138225	2	AL139822	Homo sapi
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45	189.8	10.9	978	10	AY011714	Myocastor

# ALIGNMENTS

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ACCESSION	AX085543				
VERSION	AX085543.1	GI:13275577			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 1734)				
JOURNAL	Erickson, J., Goddard, J.G., Kiefer, M. and Picker, D.				
FEATURES	Compounds which modulate the activity of an lpa receptor				
source	Patent: WO 0112838-A 6 22-FEB-2001;				
	Atairgin Technologies, Inc. (US)				
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BASE COUNT 302 a 543 c 506 g 383 t
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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LOCUS
DEFINITION Homo sapiens G protein-coupled receptor Edg-4 mRNA, complete cds.
ACCESSION AF011466
VERSION AF011466.1 GI:2735848
SOURCE human.
ORGANISM Homo sapiens

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29-JUL-1998



us-09-274-752d-2.rge

[illegible]





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RESULT 5  
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 LOCUS Homo sapiens lysophosphatidic acid G protein-coupled receptor 4  
 DEFINITION (EDG4) mRNA, complete cds.  
 ACCESSION AF233092  
 VERSION AF233092.1 GI:7243675  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1159)  
 Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.  
 Lysophosphatidic acid (LPA) receptors of the EDG family are  
 differentially activated by LPA species. Structure-activity  
 relationship of cloned LPA receptors  
 FEBS Lett. 478 (1-2), 159-165 (2000)  
 20382744  
 2 (bases 1 to 1159)  
 Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.  
 Direct Submission  
 Submitted (09-FEB-2000) Graduate School of Pharmaceutical Sciences,  
 The University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033,  
 Japan

FEATURES  
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BASE COUNT 183 a 394 c 325 g 257 t  
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L	361	GTGGCCACACTGCTGGCCATCGCCGTGGAGCGCACCGCAGTGTGATGGCCGTGCAGCTG	420
Qy	499	cacagccctctgccccgtggccgcggtggtcatgctcatctgtgggcgtgtgggtggtcgc	558
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Qy	559	ctggcctggggctgctgctgccactcctggcactgcctctgtgccctggaccctgc	618
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L	781	GTGTGTACTGTCTCTGGATGGTTTAGGCTGTGAGTCTCTGCAATGCTCTGGCTGTAGAAAAG	840
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Qy	979	gatgctgagatgcgcgcgaaccttcgcgcgcctctctgtgcgctgtgcctcccgcaatcc	1038
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Qy	1039	accgcggagtctgtccactatatacctctgcgcagggaggtgcagacactgcatactg	1098
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Qy	1099	cttcccgagacggccaccactgat-gactccaccttagctactcctgaactcagcg	1157
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Qy	1158	gtacgcggcaagcaacaaatccacagccctgatgactgtgggtgctcctgcgtccaacc	1217
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RESULT      6
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LOCUS
DEFINITION Homo sapiens DNA from chromosome 19-cosmid R33799, genomic
            sequence, complete sequence.
AC002306
VERSION     AC002306.1 GI:2213634
KEYWORDS    HTG.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 38651)
AUTHORS    Lamerdin,J.E., McCreedy,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
            Garcia,E., Kyle,A., Ramirez,M., Stillwagen,S., Garnes,J.,
            Dangnan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
            Olsen,A.O. and Carrano,A.V.
            anonymous cosmid from 19p12
            unpublished (1997)
REFERENCE   2 (bases 1 to 38651)
AUTHORS    Lamerdin,J.E.
TITLE      Direct Submission
JOURNAL    Submitted (24-JUN-1997) Human Genome Center, Lawrence Livermore
            National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
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Db 3025 TC 3024

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## RESULT 8

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AR092424 AR092424 2185 bp DNA PAT 08-SEP-2000
LOCUS Sequence 3 from patent US 5998164.
DEFINITION AR092424
ACCESSION AR092424
VERSION AR092424.1 GI:10019178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REF"RENCE 1 (bases 1 to 2185)
TORS Li,Y.,Cao,L., Ni,J., Gentz,R., Bult,C.J., Sutton,G.G. III and
Rosen,C.A.
TITLE Polynucleotides encoding human G-protein coupled receptor GPR2
JOURNAL Patent: US 5998164-A 3 07-DEC-1999;
FEATURES Location/Qualifiers
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Source /organism="unknown"
BASE COUNT 413 a 621 c 696 g 455 t
ORIGIN

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Query Match 49.6%; Score 860.4; DB 6; Length 2185;
Best Local Similarity 97.9%; Pred. No. 3.1e-154;
Matches 914; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

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Qy 1129 ccacccttagctactctgaacttcagcgtgacgcgcgcgcgcgcgcgcgcgcgcgcgc 1188
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Qy 1189 gatgactgtgggtgctcctgggtcaccaccccaacc 1222
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## RESULT 9

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DEFINITION unordered pieces.
ACCESSION AC073687
VERSION AC073687.1 GI:8810304
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus...
REFERENCE 1 (bases 1 to 201331)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse

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Qy	340	ctcttctcattgttcacaactggtccccgcacgccgcgactttcacttgagggtcgtgttc	399
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DEFINITION	Rattus norvegicus endothelial differentiation gene 2 (Edg-2) mRNA complete cds.				
ACCESSION	AF014418				
VERSION	AF014418.1	GI:2623061			
KEYWORDS					
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
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RESULT 15







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 QY 243 VVILGAFVVCWTPGVVLLDGLGCESCNCVLAKEYFLLAEANSLVNAAYVSCRDSEM 302  
 Db 241 VMTVLGAFVVCWTPGVVLLDGLGCESCNCVLAKEYFLLAEANSLVNAAYVSCRDSEM 300  
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 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
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 GN EDG7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RP SEQUENCE FROM N.A.  
 RA Lynch K.R., Im D.-S.;  
 RT "Molecular cloning of a lysophosphatidic acid receptor, LP-A3/Edg-7.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99419064; PubMed=10488122;  
 RA Bandoh K., Aoki J., Hosono H., Kobayashi S., Kobayashi T.,  
 RA Murakami-Murofushi K., Tsujimoto M., Arai H., Inoue H.;  
 P' "Molecular Cloning and Characterization of a Novel Human G-Protein-  
 Coupled Receptor, EDG7, for Lysophosphatidic Acid.";  
 J. Biol. Chem. 274:27776-27785(1999).  
 DR EMBL; AF186380; AAF00530.1;  
 DR EMBL; AF127138; AAD56311.1;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1.1;  
 DR PRINTS; PR00237; GPCRHOOPS.  
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 SQ SEQUENCE 353 AA; 40128 MW; 105DC9DD185E2CE7 CRC64;

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Db 121 LVIAVERHRSVMVQLHSLRPRGRVVMVIGVWVAALGLGLLPAHSHWCLCALDRCSMA 180  
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 Db 241 VMTVLGAFVVCWTPGVVLLDGLGCESCNCVLAKEYFLLAEANSLVNAAYVSCRDSEM 300  
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 Db 301 YNTMRKMICCA-LODSNTE 318  
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 Db 349 NKSTS 353

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 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
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 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20351181; PubMed=10891327;  
 RA Fitzgeraid L.R., Dytko G.M., Sarau H.M., Mannan I.J., Ellis C.,  
 RA Lane P., Tan K.B., Wilson S., Bergsma D.J., Ames R.S., Foley J.J.,  
 RA Campbell D., McMillan L., Evans N., Elshourbagy N., Tsui P.;  
 RT "Identification of an EDG7 Variant, HOFNH30, a G-Protein-Coupled  
 Receptor for Lysophosphatidic Acid.";  
 RL Biochem. Biophys. Res. Commun. 273:805-810(2000).  
 DR EMBL; AF236117; AAF91291.1;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1.1;  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 354 AA; 40339 MW; A70ED5CFA6F7D706 CRC64;

Query Match 43.1%; Score 849; DB 4; Length 354;  
 Best Local Similarity 46.8%; Pred. No. 1.9e-58;  
 Matches 162; Conservative 62; Mismatches 104; Indels 18; Gaps 2;

QY 4 MGOCYNETIGFFYNNSGKELSSHW- PKDVVVVALGLTVSVLLNLLVIAAASNR 62  
 Db 1 MNECHDKHMDFFYNRSNTDVTDDWTKLVILCVGTFCLFFFSNLSVIAAVIKNRK 60  
 QY 63 FHQPIYLLGNLAADLAFAGVAYFLFMFHTGPTARLSLEGWFLRQGLDTSLTASVATL 122  
 Db 61 FHFPFYLLANLAAADLAFAGVAYFLFMFHTGPTARLSLEGWFLRQGLDTSLTASVATL 120  
 QY 123 LAIAVERHRSVMVQLHSLRPRGRVVMVIGVWVAALGLGLLPAHSHWCLCALDRCSMA 182  
 Db 121 LVIAVERHRSVMVQLHSLRPRGRVVMVIGVWVAALGLGLLPAHSHWCLCALDRCSMA 180  
 QY 183 PLLSRSLAYLWALSLLVFLMVAAYTRIFFVVRVQMAHVSCHPRYRTTSLVKT 242  
 Db 181 PIYSRSLVFTVSNLMAFLIMVYVIRYVVRKTNVLSPHSGSISRRTPMKLMT 240  
 QY 243 VVILGAFVVCWTPGVVLLDGLGCESCNCVLAKEYFLLAEANSLVNAAYVSCRDSEM 302  
 Db 241 VMTVLGAFVVCWTPGVVLLDGLGCESCNCVLAKEYFLLAEANSLVNAAYVSCRDSEM 300



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QY 303 RTFRRLCC-----ACLRQSTRESVHYTSSAOG 331
| : : : : | | : : : |
Db 301 YSTMKKMICFCQERNLDRSRPSTILSRDSTGSGYKEDSSOG 346
| : : : : | | : : : |

RESULT 11
Q9ESJ6 PRELIMINARY; PRT; 345 AA.
AC Q9ESJ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR SNGPCR32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX SEQUENCE FROM N.A.
RP STRAIN-HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
R "Identification and characterization of novel G-protein coupled
R receptors expressed in regenerating peripheral nerve.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097733; AAG24262.1;
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; P00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1.2; 1.
KW Receptor.
SQ SEQUENCE 345 AA; 39137 MW; CF3BEF46EB35046A CRC64;

Query Match 42.8%; Score 842; DB 11; Length 345;
Best Local Similarity 46.6%; Pred. No. 6.4e-58;
Matches 166; Conservative 64; Mismatches 110; Indels 16; Gaps 4;

QY 15 FFYNSGKELSHWR-PKDVVVAALGLVSVLVLTNLVIAAASNRFFHQPIYLLGN 73
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 3 FFYNSRNTDADEWTGTLKVLVLCVFTFCFFIFFSNLSLVIAAVITNRKFFPFYLLAN 62
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 74 LAADLFAGVAYFLMFHTGPTARLTLEGWFLRGLDTSLTASVATLLAIVERHRSV 133
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 63 LAVADFFAGIAYVLFMFHTGPTARLTLEGNWLLRGLDTSLTASLANLVIAVERHRSI 122
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 134 MAVQLHSLRPRGVVVLGVVVAALGLGLLPAHSHWCLALDRCSMAPLLSRSYLAW 193
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 123 MMRTHSNLTKRVTLILLVWAIEMFAGVPTLGNWCLNCSACSLAPIYSRYLIFW 182
| : : : : | | : : : | | : : : | | : : : | | : : : |

C 194 ALSLLVLLMVAVYTRIFFVRRVQRMARHVSCHPRRETTLSLVKTVIILGAFVVC 253
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 183 TVSNLLAFFIMVVVRYIMYKRYKNTLVSPHTSGSISRRRAPMKMTKMTVVLGAFVVC 242
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 254 WTPGVLLLDGLGCESCNLVAVEYFELLAEANSLVAAVYSCRDSEMRRTFRLLCCA 313
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 243 WTPGLVLLLDGLGNQCNQVHKRWFLLLALLNSVMPPIIYSYKDEMYNTMRMICA 302
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 314 CLRQSTRESVHYTSSAOGGASTRIMLPENGHPLMTPPFSYLE--LQRYAASNKSTA 367
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 303 -----PIDSNARHPS---RIPSTIHSRSDTSGQYLEDISQGVQCNKSSS 345
| : : : : | | : : : | | : : : | | : : : | | : : : |

RESULT 12
Q99NQ8 PRELIMINARY; PRT; 326 AA.
AC Q99NQ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE EDG1 (FRAGMENT).
GN EDG1.
```

```
Myocastor coypus (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011714; AAK01982.1; -.
FT NON_TER 1
FT NON_TER 326
SQ SEQUENCE 326 AA; 36357 MW; 18963183FB9742FF CRC64;

Query Match 28.3%; Score 556.5; DB 11; Length 326;
Best Local Similarity 36.6%; Pred. No. 1e-35;
Matches 121; Conservative 70; Mismatches 111; Indels 29; Gaps 6;

QY 40 LTVSVLVLTNLVIAAASNRFFHQPIYLLGNLAADLFAGVAYFLMFHTGPTARL 99
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 13 ILICCLILLENVFLVLTWKTKFHRPMYFFIGNLALSLLAGVAVIANLLSGTTTYRL 72
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 100 SLEGWFLRGLDTSLTASVATLLAIVERHRSVMAVQLHSLRPRGVVVLGVVVAAL 159
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 73 TLVQWFLREGSMFVALSASFVLSLLAIAIERITYITMLKMLHNGSNNSRFLLSGCGWAISL 132
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 160 GIGLLPAHSHWCLALDRCSMAPLLSRSYLAVWALSLLVFLMVAVYTRIFFYVRRV 219
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 133 ILGGLPIMGWNCVDALPSCSTVLPYKHYILFCTVFTLLIALLAIVILCRIYSLVTRTS 192
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 220 QMA--EHVSHPRYRETTLSLVKTVIILGAFVVCWPGQVVLVDGLGC--ESCNVLA 275
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 193 RRLTRKNKASKASRSRSEKSLALLKTVIIVLSAFIACWAPLFIILLD-VCKVKTCIDLY 251
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 276 VEKYFLLAEANSLVAAVYSCRDSEMRRTFRLL--CCACLROSTRESVHYTSSAOGGAS 334
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 252 KAEYELVLAVLNSGTNPVIITNKRMRRAFIMVSCCKC-----SGG-- 294
| : : : : | | : : : | | : : : | | : : : | | : : : |

QY 335 TRIMLPENGHPLMTPPFSYLELQRYAASNKS 365
| : : : : | | : : : | | : : : | | : : : | | : : : |
Db 295 -----DSAGIKRPIIAGVFRSRSKSDNS 319
| : : : : | | : : : | | : : : | | : : : | | : : : |

RESULT 13
Q9BF48 PRELIMINARY; PRT; 326 AA.
AC Q9BF48;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE EDG1 (FRAGMENT).
GN EDG1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011733; AAK02001.1; -.
FT NON_TER 1
FT NON_TER 326
SQ SEQUENCE 326 AA; 36691 MW; C3257E28D83B88FA CRC64;
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Query Match 27.9%; Score 549.5; DB 6; Length 326;  
Best Local Similarity 36.0%; Pred. No. 3.5e-35;  
Matches 121; Conservative 69; Mismatches 117; Indels 29; Gaps 6;

QY 40 LTVSVLVLTLLNLVIAAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARL 99  
Db 13 ILCCFIILNFIENFVLTITWTKKFRHPMYFIGNLALSDLLAGVAYTANLLSGATYKL 72  
QY 100 SLEGWFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAAL 159  
Db 73 TPAQWFLREGSMFVALSASFVSLAIAIERIYITMLKMLHNGSNRFRSFLDISACWISL 132  
QY 160 GLGLPAHSHWCLCALDRCRMAPLRSYLAVALSSLLVFLMVAVYTRIFFYVRRV 219  
Db 133 ILGLPLMGWNCISTLPSCTVPLVYKHVILFCTVFTLLLAIVILYCRISLVRTS 192  
QY 220 QRNA--EHVSCHPRYRTTSLVKTVVIIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 275  
L 193 RLUTFRKNISKASRSSEKSLALLKTVIIVLGVFACWAPLFIILLD-VGCKVKTCDILF 251  
QY 276 VEKYPFLAANSLVNAVYSCDSEMRRTFRLL-CCACLRQSTRESVHYTSSAOGAS 334  
Db 252 RTEYFLVAVNSGTNPPIITLSNKMRRAPVRIMSCCKC-----PSGDSAGKF 300  
QY 335 TRIMLPENGHPLMTPTPPSYLELQRYAASNKSTAPDD 370  
Db 301 TR-----PIAGMEFSSKSDNSHPQKD 324

RESULT 14  
Q9BF52  
ID Q9BF52 PRELIMINARY; PRT; 326 AA.  
AC Q9BF52;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE EDG1 (FRAGMENT).  
GN EDG1.  
OS Megaptera novaeangliae (Humpback whale).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
OC Balaeopteridae; Megaptera.  
OX NCBI\_TaxID=9773;  
RN [1]  
RP SEQUENCE FROM N.A.  
F MEDLINE-21082082; PubMed-11214319;  
R Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RT O'Brien S.J.;  
RL "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011729; AAK01997.1; -  
FT NON\_TER 1  
FT 326  
SQ SEQUENCE 326 AA; 36661 MW; 8886296016C185B1 CRC64;

Query Match 27.9%; Score 548.5; DB 6; Length 326;  
Best Local Similarity 36.5%; Pred. No. 4.2e-35;  
Matches 122; Conservative 67; Mismatches 116; Indels 29; Gaps 6;

QY 42 VSVLVLTLLNLVIAAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARLSL 101  
Db 15 ICCFIILNFIENFVLTITWTKKFRHPMYFIGNLALSDLLAGVAYTANLLSGATYKLTTP 74  
QY 102 EGMFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAALGL 161  
Db 75 AQWFLREGSMFVALSASFVSLAIAIERIYITMLKMLHNGSNRFRSFLDISACWISL 134  
QY 162 GLPLPAHSHWCLCALDRCRMAPLRSYLAVALSSLLVFLMVAVYTRIFFYVRRVOR 221  
Db 135 GGLPIMGWNCISALPSCSTVPLVYKHVILFCTVFTLLLSIVILYCRISLVRTSRR 194  
QY 222 MA--EHVSCHPRYRTTSLVKTVVIIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 277

Db 195 LTFERNISKASRSSEKSLALLKTVIIVLGVFACWAPLFIILLD-VGCKVKTCDILFRT 253  
QY 278 KYFLLLAANSLVNAVYSCDSEMRRTFRLL-CCACLRQSTRESVHYTSSAOGASR 336  
Db 254 EYFLVAVNSGTNPPIITLSNKMRRAPVRIMSCCKC-----PSGDSAGKFTR 302  
QY 337 IMLPENGHPLMTPTPPSYLELQRYAASNKSTAPDD 370  
Db 303 -----PIAGMEFSSKSDNSHPQKD 324

RESULT 15  
Q99NR2  
ID Q99NR2 PRELIMINARY; PRT; 326 AA.  
AC Q99NR2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE EDG1 (FRAGMENT).  
GN EDG1.  
OS Dipodomys heermanni (Kangaroo rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Heteromyidae;  
OC Dipodomysinae; Dipodomys.  
OX NCBI\_TaxID=10018;  
RN [1]  
RP SEQUENCE FROM N.A.  
XX MEDLINE-21082082; PubMed-11214319;  
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RA O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011710; AAK01978.1; -  
FT NON\_TER 1  
FT 326  
SQ SEQUENCE 326 AA; 36486 MW; FA9C24567F402E21 CRC64;

Query Match 27.7%; Score 546; DB 11; Length 326;  
Best Local Similarity 40.0%; Pred. No. 6.6e-35;  
Matches 112; Conservative 65; Mismatches 97; Indels 6; Gaps 4;

QY 40 LTVSVLVLTLLNLVIAAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARL 99  
Db 13 ILICLIILNFIENFVLTITWTKKFRHPMYFIGNLALSDLLAGVAYTANLLSGATYKL 72  
QY 100 SLEGWFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAAL 159  
Db 73 TPAQWFLREGSMFVALSASFVSLAIAIERIYITMLKMLHNGSNRFRSFLDISACWISL 132  
QY 150 GLGLPAHSHWCLCALDRCRMAPLRSYLAVALSSLLVFLMVAVYTRIFFYVRRV 219  
Db 133 ILGLPIMGWNCISALPSCSTVPLVYKHVILFCTVFTLLLSIVILYCRISLVRTS 192  
QY 220 QRNA--EHVSCHPRYRTTSLVKTVVIIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 275  
Db 193 RLUTFRKNISKASRSSEKSLALLKTVIIVLGVFACWAPLFIILLD-VGCKVKTCDILF 251  
QY 276 VEKYPFLAANSLVNAVYSCDSEMRRTFRLL-CCAC 314  
Db 252 KAEYFLVAVNSGTNPPIITLSNKMRRAPVRIMSCCKC 291

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Job time: 2340 sec

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Date: Dec 20, 2001 12:02 PM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-325-897-1	1	849.00	1752.40	5.8e-90	1065
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-997-803-3	1	589.50	1212.77	6.7e-60	639
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-196-989B-3	1	539.50	1091.69	3.7e-53	2232
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-842-238-9	1	499.50	1016.06	6.0e-49	1137
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-196-989B-1	1	498.00	1001.68	3.8e-48	2754
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-760-936-1	1	498.00	1001.68	3.8e-48	2754
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-097-231-17	1	327.00	654.95	7.9e-29	978
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-842-045-9	1	326.00	652.88	1.0e-28	975
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-842-238-9	1	326.00	652.88	1.0e-28	975
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-672-109B-5	1	300.00	596.87	1.3e-25	1080
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-842-045-5	1	300.00	596.87	1.3e-25	1080
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-842-238-5	1	300.00	596.87	1.3e-25	1080
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-629-335B-5	1	300.00	596.87	1.3e-25	1080
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-706-281A-11	1	294.00	581.53	9.7e-25	1338
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-097-231-11	1	294.00	581.53	9.7e-25	1338
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-044-812A-3	1	292.00	577.32	1.7e-24	1338
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-861-747-1
seq documentation block:
Sequence 1, Application US/08861747
Patent No. 6020158
GENERAL INFORMATION:
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 15th St., NW, Suite 330 - G Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,747
FILING DATE: 22-MAY-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jahns, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: P8074-7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1761 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-861-747-1
alignment_scores:
Quality: 1941.00 Length: 383
Ratio: 5.094 Gaps: 1
Percent Similarity: 99.478 Percent Identity: 98.956
alignment block:
US-09-274-752D-1 x US-08-861-747-1
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141 TAACAACAGTGCACCAAGAGCTCAGCTCCACTGGGGCCCAAGATGTTGG 190
34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuThrAsn 50
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alignment_scores:
  Quality: 1941.00      383
  Ratio: 5.094
  Percent Similarity: 99.478  Percent Identity: 98.956

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17 rAsnAsnSerGlyLysGluLeuSerSerHisTrrArgProLysAspValV 34
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227 TTACAACAGTGGCAAGAGCTCAGCTCCACTGGCGGCCCAAGAGATGG 276
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34 aIValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
|||||
277 TCGTGTGGCACTGGGCGCTGACCGCTCAGCGTGTGGTGTGTGCTGACCAAT 326
|||||
51 LeuLeuValIleAlaIleAlaSerAsnArgArgPheHisGlnProI 67
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327 CTGCTGGTGCATAGCAGCCATCGCTCCAAACGCCGCTTCCACCAGCCCAT 376
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67  eTyrTyrLeuLeuGlyAsnLeuAlaAlaAspLeuPheAlaGlyVala 84
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377 CTACTACTCTGCTGGCAATCTGGCGCGGCTGACCTCTTCGGGGCGTGG 426
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427 CCTACTCTTCTCTCATCTTCACACTGGTCCCGCACAGCCGCACTTTCA 476
101 LeuGluGlyTrpPheLeuArgGlnGlyLeuLeuAspThrSerLeuThrAl 117
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167 sSerTrpHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
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184 euLeuSerArgSerTyrLeuAlaValTrpAlaLeuSerSerLeuLeuVal 200
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727 TGCTCAGCGCTCTCTATTGGCCGCTGTGGGCTGTGTCGAGCGCTGTTGTC 776
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217 qArgValGlnArgMetAlaGluHisValSerCysHisProArgTyrArgG 234
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seq_documentation_block:
Sequence 1, Application US/08789982
Patent No. 6037146
GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Bergsma, Derk
TITLE OF INVENTION: CDNA CLONE HE8CH90 THAT ENCODES
A NOVEL 7- TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08789,982
APPLICATION NUMBER: US/08789,982
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-789-982-1

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Ratio: 5.104 Gaps: 1
Percent Similarity: 99.734 Percent Identity: 99.468

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183 TAACAAACAGTGGCAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGG 232
34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
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233 TCGTGTGGCTGCTGGGCTGACCGTGCAGCGTGTGCTGTGCTGACCAAT 282

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333 CTACTACCTGCTGGGCAATCTGGCCGCGCTGACCTCTTCGGCGGGCTGG 382  
84 laTyrLeuPheLeuMetPheHisThrGlyProArgThrAlaArgLeuSer 100  
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seq\_documentation\_block:

Sequence 3, Application US/08467948A  
Patent No. 5998164  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
Coupled Receptor GPR2  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 884..2062  
US-08-467-948A-3

alignment\_scores:

Quality: 1484.50 Length: 359  
Ratio: 4.582 Gaps: 6  
Percent Similarity: 90.251 Percent Identity: 86.072

alignment\_block:

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44 alleuVal.....LeuLeuThrAsnLeuLeuValIleAlaIle 57  
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58 AlaSerAsnArgArgPheHisGlnProIleTyrTyrLeuLeuGlyAsn 74  
1097 ..... : : : : :CTCGCGCCAATCT 1110  
74 uAlaAlaAlaAspLeu\_PheAlaGlyValAlaTyrLeuPheLeuMetPhe 90  
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1210 GCAGGGCTGTGTGGACACAACCCTCAGTCGCTCGGTGGCGCACACTGCTG 1259  
124 lAlleAlaValGLuArgHisArgSerValMetalVaIGlnLeuHisSer 140  
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141 ArgLeuProArgGlyArgValValMetLeuIleValGlyValTrpValAl 157  
1310 CGCTGCCCGTGGCGCGGTGGTCAATGCTCATGTTGGCGGTGTGGGTGGC 1359  
157 aAlaLeuGlyLeuGlyLeuLeuProAlaHisSerTrpHisCysLeuCysA 174  
1360 TGCCCTGGCGCTGGGGTGTGCTCGCTGCCACTCTCTGGGCAGTCCCTCTGTG 1409  
174 lAlaLeuAspArgCysSerArgMetalProLeuLeuSerArgSerTyrLeu 190  
1410 CCTCTGGACCGCTCTCAGCATGGCACCCCTGCTCAGCGCTCTATTGTG 1459  
191 AlavalTrpAlaLeuSerSerLeuLeuValPheLeuLeuMetValAlaVa 207  
1460 GCCGTCTGGGCTCTGTGAGCCTGCTTGTCTTCTTCGTCATGGTGGCTGT 1509  
207 lTyrThrArgIlePhePheTyrValArgArgValGlnArgMetAlag 224  
.510 GTACACCGCATTTTCTTCTACGTGCGCGCGAGTGAGCGCATGGCAG 1559  
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241 LysThrValValIleIleLeuGlyAlaPheValValCystTrpThrProGI 257  
1610 AAGACTGTGTGCATCATCTCTGGGGCGGTTCGTGGTCTGCTGGACACCAG 1659  
257 yGlnValValLeuLeuLeuAspGlyLeuGlyCysGluSerCysAsnVal 274  
1660 CCAGGTGGTACTGCTCCTCGATGGTTTTAGGCTGTGAGTCTTCGCAATGTCC 1709  
274 euAlaValGluLysTyrPheLeuLeuLeuAlaGluAlaAsnSerLeuVal 290  
1710 TGGCGTTAGAAAAGTAGTTCTTCCGAGATGCTGAGATGGCGCGACCTTCGG 1759  
291 AsnAlaAlaValTyrSerCysArgAspSerGluMetArgArgThrPheAr 307  
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1910  CGAGAAGCGCCACCCACTGATGCAGCTCCACCTTTAGCTACCTTGACACTA 1959
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357  GlnArgTyrAlaAlaSerAsnLysSerThrAlaProAspAspLeuTrpVa 373
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seq_documentation_block:
: Sequence 3, Application US/08467947A
: Patent No. 6090575
: GENERAL INFORMATION:
: APPLICANT: LI, YI
: APPLICANT: CAO, LIANG
: APPLICANT: NI, JIAN
: APPLICANT: GENTZ, REINER
: APPLICANT: BULT, CAROL J.
: APPLICANT: SUTTON III, GRANGER G.
: APPLICANT: ROSEN, CRAIG A.
: TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
: TITLE OF INVENTION: Coupled Receptor GPR1
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVE., NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/467,947A
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04079
: FILING DATE: 30-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: STEFFE, ERIC K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 3

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alignment_scores:
  Quality: 1484.50
  Ratio: 4.582
  Length: 359
  Gaps: 6
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Percent Similarity: 90.251 Percent Identity: 86.072

## alignment\_block:

US-09-274-752D-1 x US-08-467-947A-3

Align seg 1/1 to: US-08-467-947A-3 from: 1 to: 2185

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44 aLeuVal.....LeuLeuThrAsnLeuLeuValIleAlaIle 57
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1047 GTTTGCTCCCTCCCTCCATTAACCACTGACGTGTGCCAGCTGAAGTAACT 1096
58 AlaSerAsnArgPheHisGlnProIleTyrTyrLeuLeuGlyAsnLe 74
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1097 .....CTCGCGGCCCAATCT 1110

74 uAlaAlaAlaAspLeuPheAlaGlyValAlaTyrLeuPheLeuMetPhe 90
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seq_documentation_block:
; Sequence 1, Application US/08763938
; Patent No. 6140060
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: HECHT, Jonathan H.
; TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
; STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,938
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-6018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-763-938-1
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Percent Similarity:	77.717	Percent Identity:	53.804

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seq_documentation_block:
Sequence 1, Application PC/TUS9610618
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0042 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Rheumatoid Synovium

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Patent No. 6057126
GENERAL INFORMATION:
APPLICANT: CHUN, Jerold J.M.
APPLICANT: GUPTA, Ashwani
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1322
US-08-997-803-12
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186 erArgSerTrValAlaValTrpAlaLeuSerSerLeuValPheLeu 202
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811 GCAGGAGTTACTTGTCTTCTGGACAGTGTCCAACTCATGCGCTTCCTC 860
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203 LeuMetValAlaValTyrThrArgIlePhePheTyrValArgArgVa 219
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861 ATCATGTTGTGGTGTACCTGCGGATCTACGTGTACGTCAAGAGGAAAC 910
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219 lGlnArgMetAlaGluHisValSerCysHisProArgTyrArgGluThrT 236
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911 CAACGCTTCTCTCCGATCAACAGTGGTCCATCAGCCGCGGAGGACAC 960
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236 hrLeuSerLeuValLysThrValValIleLeuGlyAlaPheValVal 252
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253 CysTrpThrProGlyGlnValValLeuLeuLeuAspGlyLeuGlyCysGl 269
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1011 TGCTGGACCCCGCGCTGTGTCTTCTGCCCTCGACGCGCTGAACCTGAC 1060
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286 laAsnSerLeuValAsnAlaAlaValTyrSerCysArgAspSerGluMet 302
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; Sequence 1, Application US/09325897
; Patent No. 6242572
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; APPLICANT: Catherine E. Ellis
; APPLICANT: Ganesh M. Sathe
; APPLICANT: Stephanie Van Horn
; APPLICANT: Robert S. Ames
; APPLICANT: James J. Foley
; APPLICANT: Laura R. Fitzgerald
; APPLICANT: Harry M. Sarau
; APPLICANT: Jonathon K. Chambers
; TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: GH70014-2
; CURRENT APPLICATION NUMBER: US/09/325,897
; EARLIER APPLICATION NUMBER: 09/215,072
; EARLIER FILING DATE: 1999-06-04
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/992,031
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 60/046,366
; EARLIER FILING DATE: 1997-05-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Human
; US-09-325-897-1
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  Quality: 849.00      Length: 346
  Ratio: 3.216         Gaps: 2
  Percent Similarity: 76.301  Percent Identity: 46.821

alignment_block:
US-09-274-752D-1 x US-09-325-897-1 ..
Align seg 1/1 to: US-09-325-897-1 from: 1 to: 1065

4 MetGlyClnCysTyrTyrAsnGluThrIleGlyPhePheTyrAsnAsnSe 20
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1 ATGAATGAGTGTCACTATGACAAAGACATGGACTTTTATATATAGGAG 50
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alignment_scores:
  Quality: 589.50      Length: 208
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  US-09-274-752D-1 x US-08-997-803-3  ..

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107  gCInGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLeuLeuA 124
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151 AACTTGACCAAAAGCGGTGACGCTGCTATTCTGCTGCTGGGCAT 200  
157 aAlaLeuGlyLeuLeuLeuProAlaHisSerTrpHisCysLeuCysA 174  
201 CGCATCTTTCATGGGGCGGCGCCACACNCTGGGATGGGATTCCTGC 250  
174 laLeuAspArgCysSerArgMetAlaProLeuLeuSerArgSerTrp 190  
251 ACATCTGGGCTGCTCTCTGCTGCTCCATTTACAGTAGGAGTACCTC 300  
191 AlaValTrpAlaLeuSerSerLeuLeuValPheLeuLeuMetValAla 207  
301 ATTTTCTGGAGCTGTCTCAACCTCTGGCTTCTTTCATCATGCTGG 350  
207 lTyrThrArgIlePhePheTyrValArgArgValGlnArgMetAlaG 224  
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224 luHisValSerCysHisProArgTyrArgGluThrThrLeuSerLeu 240  
401 CACACACAGCTGGCTCCATCAGCGCGGAGGGCTCCCATGAGTAATG 450  
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601 AACCCCTCATCTAC...TGCCGC 621

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seq\_documentation\_block:  
; Sequence 3, Application US/08196989B  
; Patent No. 5585476  
; GENERAL INFORMATION:  
; APPLICANT: MacLennan, A. John  
; TITLE OF INVENTION: Molecular Cloning and Expression of  
; TITLE OF INVENTION: G-Protein Coupled Receptors  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/196,989B  
; FILING DATE: 15-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lloyd, Jeff

REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: MAC-100  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 269..1420  
US-08-196-989B-3  
alignment\_scores:  
Quality: 539.50 Length: 308  
Ratio: 2.581 Gaps: 6  
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alignment\_block:  
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28 pargProLysAspValValValAlaLeuGlyLeuThrValSerValL 45  
406 TAAACTGACTTCAGTGGTGTTCATT.....CTCATCTGCTGCT 443  
45 euValLeuLeuThrAsnLeuValIleAlaIleAlaSerAsnArg 61  
444 TCATCATCTAGAGATATATTTGCTTCTTAACATTTGGAAACCAAG 493  
62 ArgPheHisGlnProIleTyrLeuLeuGlyAsnLeuAlaAlaAs 78  
494 AAGTTCCACCGCGCCATGACTATTTTCATAGGCAACCTAGCCCTCTCGGA 543  
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544 CTGTGTAGCAGGAGTGGCTTACACAGCTAACCTGCTGTCTGTGGGCCA 593  
95 rgThrAlaArgLeuSerLeuGluGlyTyrPheLeuArgGlnGlyLeu 111  
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112 AspThrSerLeuThrAlaSerValAlaThrLeuLeuAlaIleAlaValG 128  
644 TTTGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693  
128 uArgHisArgSerValMetAlaValGlnLeuHisSerArgLeuProArg 145  
694 GCGCTACATCACCATGCTGAAGATGAACATACACACGCGCACAGCT 743  
145 lyArgValValMetLeuIleValGlyValTrpValAlaAlaLeuGly 161  
744 CGCGCTCTCTTCTGCTGATCAGTGGCTGCTGCTGCTGCTGCTGCTG 793  
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; NAME/KEY: CDS

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3	1880	96.9	1889	3	US-08-861-747-3	Sequence 3, Appli
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5	860.4	49.6	2185	2	US-08-467-948A-3	Sequence 3, Appli
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7	364	21.0	2250	1	US-08-763-938-1	Sequence 1, Appli
8	324.4	18.7	1875	5	PCT-US96-10618-1	Sequence 1, Appli
9	282	16.3	1065	4	US-09-323-897-1	Sequence 1, Appli
10	278	16.0	1356	3	US-08-997-803-13	Sequence 13, Appli
11	181.8	10.5	639	3	US-08-997-803-12	Sequence 12, Appli
12	180.4	10.4	1637	3	US-08-997-803-3	Sequence 3, Appli
13	163.2	9.4	2232	1	US-08-852-824-3	Sequence 3, Appli
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## RESULT

US-08-861-747-3  
Sequence 3, Application US/08861747  
Patent No. 6020158  
GENERAL INFORMATION:  
APPLICANT: VYAS, Tejal B.  
APPLICANT: MUNROB, Donald G.  
TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nikaído, Marmelstein, Murray & Oram LLP  
STREET: 655 15th St., NW, Suite 330 - G Street Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,747  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Jahns, Kristina M.  
REGISTRATION NUMBER: 41, 092  
REFERENCE/DOCKET NUMBER: P8074-7003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 3:

b 934 GCTGGACACCAAGCCAGGTGGTACTGCTCCTGGATGGTTAGGCTGTGAGTCCTGCAATG 995

CITY: King of Prussia

STATE: PA  
COUNTRY: USA









QY	100	cagtgctactacaacagagaccatcggtcttctctatacaaacagtggcgaagagtcagc	159
Db	375	CAGTGTCTTACAACGAGTC CATTGCTTCTTTTATACCGAAGTGGAAAGCATCTGCC	434
QY	160	tcccaactggcggcccaaga gatgtgctgtgtggtcacctggggctaacgctcagcgtgctg	219
Db	435	ACAGAATGGAACACAGCTCA CGAAGCTG GTGATGGGACTTGG AATCACTGTTTATCTTC	494
QY	220	gtgctctgaaccaatctgctg tcatagacagccatcgctcca acccgcgcttcacacag	279
Db	495	ATCATGTTGGCCAACCAT TATTGGTGCATGTFGGCAATCTATGTCAACGGCGTTCCTATTT	554
QY	280	cccattctactactgctcaga aatctgacgccagagtga cttcttcacagagatcacctac	339

REGISTRATION NUMBER: 33,888

REGISTRATION NUMBER: 33,888



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1356 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-997-803-13

Query Match 16.1%; Score 279.6; DB 3; Length 1356;  
Best Local Similarity 56.6%; Pred. No. 9.4e-60;  
Matches 538; Conservative 0; Mismatches 409; Indels 3; Gaps 1;

C 74 tggagccagatggtccatcatggtggccagtgctactacaacagagaccatggcttcttct 133  
Db 16 TCACGTTCTCTCCCAATGAATGAGTGTCTACTATGACAGACATGACTTTTTTT 75  
Qy 134 ataaacaagtggcaagagtcagctcccactgg---cggcccaagagatggtgctg 190  
Db 76 ATAATAGGAGCAACACTGATCTGCTGATGACTGGACAGCAACAAAGCTTGTGATGTTT 135  
Qy 191 tggcaactggggtgacctgacgtgagtgctggtgctgacccaatctgctggtcatagcag 250  
Db 136 TGTGTGTTGGGACGTTTTTCTGCTGTTTATTTTTTTTTTCTAATCTCTGCTATCGCG 195  
Qy 251 ccactgcgtcccaacgcgcgtccaccagccactatctactacctgctgcgcaactggccg 310  
Db 196 CAGTGATCAAAACAGAAAATTCATTTCCCTTTTACTACCTTGGCTTAATTTAGCTG 255  
Qy 311 cggctgacctcttcggggcggtggcctacctctctcatgttccacactggtcccccga 370  
Db 256 CTGCGGATTTCTGCTGGAATTCCTATGTAATCTCTGATGTTTAACACAGGCCAGTTT 315  
Qy 371 cagcccgacttcaacttgagggtggttctctgctggcgaggtctgctggacacagctca 430  
Db 316 CAAAAAATTGACTGTCAACCGCTGTTTCTCGTCAAGGGCTTCCTGGACAGTAGCTGA 375  
Qy 431 ctgctcgggtggccacactgtggccactgcgcgtgagtgagtgcaaccagtgatgtccg 490  
Db 376 CTGCTTCCCTCCACCAACTTCTGGTATCCCGTGGAGAGGCACATCTCAATCATGAGGA 435  
C 491 tgcagctgcacagcgcctgcgcgcgtggccgctggtgctgctgctgctgctgctggtg 550  
Db 436 TCGCGGTCCATAGCAACCTGACCAAAAGAGGCTGACATGCTCATTTTCTGTTGCTGGG 495  
Qy 551 tggctgcccctggcgtgggtgctgctgcccactcctggcactgcctctgtgcccctg 610  
Db 496 CCATCGCATTTTATGGGGCGGTCCTCCACACTGGGCTGGAATTCCTCTGCAACATCT 555  
Qy 611 accgctgcagcatggcaccctcgtcagccctcctatattggcgtctgggctctgt 670  
Db 556 CTGCTGCTCTTCCCTGGCCCCCATTTACAGCAGGAGTTACCTTGTGTTCTGGACAGTGT 615  
Qy 671 cgagctctgtcttctctgctcagtggtgctgtgtacacccgcatcttctctcagctgc 730  
Db 616 CCAACCTCATGGCCCTTCCTCATATGTTGTTGTGTACCTGGGAGTCTACGTTGACGTCA 675  
Qy 731 ggcgcgagtgagcgcagcatggcagagcatgtcagctgcccaccccgctaccgagagacca 790  
Db 676 AGAGGAAAACCAACGCTTGTCTCCGCATACAGTGGGTCCATCAGCCCGCGGAGGACAC 735  
Qy 791 cgctcagcctggtcagactgtgtcactcactcctggggcggttcgtggtctgctggacac 850  
Db 736 CCATGAAGCTAATGAAGACGGTGTACTGTCTTAGGGCGGTTTGTGGTATGCTGGACCC 795  
Qy 851 cagccaggtggtactcctcctgagatggttttaggctgtgagtcctcgaatgctcctggctg 910  
Db 796 CGGGCTGTGTTCTGCCCCCTCGACCGGCTTGAAGTGCAGGCAGTGTGGCGTGCAGCATG 855

Qy 911 tagaaaagtacttctactgttggccgagggccaaactcactggtcaatgctgctgtact 970  
Db 856 TGAAGAAGTGGTCTCTGCTGCTGCGCTGCTCAACTCGTGTGAACCCATCATCTACT 915  
Qy 971 ctgcccagatgctgagatgctgcccgcacacttccgcgcctctctctctctgcgc 1020  
Db 916 CCTACAGGAGGAGGACATGTATGGCACCATGAAGAAGATGATCTGCTGC 965

## RESULT 10

US-08-997-803-12  
Sequence 12, Application US/08997803  
Patent No. 6057126  
GENERAL INFORMATION:  
APPLICANT: CHUN, Jerold J.M.  
APPLICANT: GUPTA, Ashwani  
APPLICANT: MUNROE, Donald G.  
APPLICANT: VIAS, Tejal B.  
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 Fifteenth Street, N.W., Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/997,803  
APPLICATION NUMBER: 08/997,803  
FILING DATE: 24-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wong, King L.  
REGISTRATION NUMBER: 37,500  
REFERENCE/DOCKET NUMBER: P8074-7020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1523 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 261..1322  
US-08-997-803-12

Query Match 16.0%; Score 278; DB 3; Length 1523;  
Best Local Similarity 56.9%; Pred. No. 2.4e-59;  
Matches 531; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

Qy 90 catcatgggcccagctactacaacagagaccatggcttctctataacaacagtgacaa 149  
Db 257 CACAATGAATGAGTGTGCTGACAGCAAGACATGGAGCTTTTTTATAATAGGACACAC 316  
Qy 150 agagctcagctcccactgg---cggcccaagagatggtgctggtggcactgggctgac 206  
Db 317 TGACTACTGCTGATGCTGGACAGCAAGACCTTGATGTTTGTGTTGTTGGAGCTT 376  
Qy 207 cgtcagcgtgctggtgctgctgacccaatctgctggtcagcagccatcgctcccaaccg 266  
Db 377 TTCTGCCCTGTTTATTTTTTTTCTAATCTCTGGTCATCGCGCAGTGATCAAAAACAG 436  
Qy 267 cgcgtccaccagcccatctactactcgtcggcaatctcgtcggcggtgacctcttcgc 326



Qy	207	cgtagcgtcgtgctgctgaccgaatctgctggtcattagcagccatcgctctcaacgcg	266
Db	433	CACTGCTGTTGATCACTAGAGCAATATTGTTCTGTCACTATTTTGGAAACCAA	492
Qy	267	ccgtccaccagcccatctactcgtctcgccaatctgcccgcgcgtcgaactcttcgc	326
Db	493	GAAGTTCACGGGCCATGACTATTTCATAGCAACCTAGCCCTCTCGACCTGTTCAC	552

Qy	207	cgtagcgtcgtgctgctgaccgaatctgctggtcattagcagccatcgctctcaacgcg	266
Db	433	CACTGCTGTTGATCACTAGAGCAATATTGTTCTGTCACTATTTTGGAAACCAA	492
Qy	267	ccgtccaccagcccatctactcgtctcgccaatctgcccgcgcgtcgaactcttcgc	326
Db	493	GAAGTTCACGGGCCATGACTATTTCATAGCAACCTAGCCCTCTCGACCTGTTCAC	552



Qy	918	gtaattcctactgttggtgcgagggccaactcaactgttcaatgtctgtctgtactctctgcg	977
Db	1153	gtaattctctgtgtgtgtgtgtgtgctgaactcaggtaccaaacccatcatctacactctgac	1212
Qy	978	agatgtgagatgcgcgcacattccgcgccttctctgctg	1019
Db	1213	caataagagagatgocccggggcttcatcaggatcatatcttg	1254

RESULT 15

```

RESULT 15
US-08-845566-2
; Sequence 2, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LINE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,566
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```

FILING DATE: 1977-01-01  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0271 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1649 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: TYMNOR01  
 CLONE: 144690

Query Match 9.3%; Score 161.4; DB 2; Length 1649;  
Best Local Similarity 53.2%; Pred. No. 1.1e-30;  
Matches 469; Conservative 0; Mismatches 387; Indels 26; Gaps 5;

[illegible]

328	GGGGCCCGCACCTTCGCTGCGCCCGCCGCGCCAGTGTGTCCTTACGGAGAGGCGCTGCTCTTC	387
421	acaagctcaactgctgcgtggtggccacactgctggccatgcgctggagc---tgcacgcgc	477
388	ACCGCCCTGGCCGCTCCACCTTCAGCCTGCTCTTCACTGACGGGAGGCGCTTGCCACC	447
478	agtgtgatgtccgtgcagctgcacacgcctgccecgtyggcgcgttggtcatgtcatt	537
448	ATGGTGGCGCGGTGGCCGAGAGCGGGGCACCAAGACACGCGCGTGTACGGCTTCATC	507
538	gtgggcgtgtggatggctgcctggccctggggctgctgcctgccaccctctggccactgc	597
508	GGCCTCTGCTGGCTGTGGCGCGCGCTGTGGGGATGCTGCCCTTTGCTGGGTGGAACTGC	567
598	ctctgtgcccctggaccgcgtctcaogcatggtcacccctgctcagcgcgtctctatttggcc	657
568	CTGTGGCGCCTTTGACCGCTGCTCCAGCCTTCTGCCCTCTACTCCAAGCGCTACATCCTC	627
658	gtctgggcctgtcgcagcctgtctcttccctgctcatgtgtgctgtgtacaccgcatt	717
628	TTCT-----GCTGTGTGATCTTCGGCGGGGCTCTGGCCACCACATCATGGCGCTC	675
718	ttcttctaogtgcggcggagtgacgcgcatggtcagagcatgtcagctgcccaccccccgc	777
676	TATGGGGCCATCTTCGCGCTGTGCAAGGCACGGGCAGAAAGGCCCCACGGCCACGGGCC	735
778	taccgagacacacgtctcagcctgtcaagactgttgtcatcatcctggggcgctcgtg	837
736	CGCGCGAAGGCC---CGCCGCTGCTGGAAGCGGTGCTGATGATCCTGCTGGCGCTTCCTG	792
838	gtctgctgacacca-----ggccaggtggactgtctcctggatggttttaggtctgga	890
793	GTGTGCTGGGGCCACTCTTCGGGGCTGCTGTGGCCGACGTCCTTTGGCTCCAACCTCTG	852
891	gtcctgcaatgtcctggctgtgaaagaagtacttctactctgttggccgaggccaaactcact	950
853	GGCCCCAGGAGTACCTCGGGGGGATGACATGATCTGTGCGCTTGGCGCGTCCCACTCGGC	912
951	ggtcaatgtctgtgtactcttgcgagatgctgagatggccgcacacttcccgcgct	1010
913	GGTCAACCCCATCTACTCTCTCCGACAGCAGGAGGTGTGCAGAGCGGTGCTCAGCCT	972
1011	t-ctctgtcgcgcgtgcctccgcgaagtccaaccgcgagctgtg	1051
973	TCCTCTGCTGCGGGTGTCTCCGGCTGGGCATGCGAGGGCCCG	1014

Search completed: December 20, 2001, 10:06:07  
Job time: 3046 sec

Result No.	Query	Score	Length	DB	ID	Description
1	1589.5	87.8	352	1	US-08-196-989B-2	Sequence 2, Appli
2	1589.5	87.8	352	2	US-08-760-936-2	Sequence 2, Appli
3	834	46.1	383	1	US-08-196-989B-4	Sequence 4, Appli
4	834	46.1	383	2	US-08-760-936-4	Sequence 4, Appli
5	823.5	45.5	381	2	US-08-845-566-3	Sequence 3, Appli
6	823.5	45.5	381	2	US-08-467-948A-28	Sequence 28, Appli
7	823.5	45.5	381	3	US-08-852-824-18	Sequence 18, Appli
8	823.5	45.5	381	3	US-08-467-947A-28	Sequence 28, Appli
9	823.5	45.5	381	5	PCT-US96-10618-4	Sequence 4, Appli
10	758	41.9	378	4	US-08-082-088-2	Sequence 2, Appli
11	749	41.4	334	1	US-08-118-270-73	Sequence 73, Appli
12	749	41.4	334	5	PCT-US93-08528-73	Sequence 73, Appli
13	526	29.1	393	5	PCT-US96-10618-3	Sequence 3, Appli
14	523	28.9	364	4	US-08-763-938-2	Sequence 2, Appli
15	523	28.9	364	5	PCT-US96-10618-2	Sequence 2, Appli
16	507	28.0	384	3	US-08-852-824-4	Sequence 4, Appli
17	490.5	27.1	354	4	US-09-325-897-2	Sequence 2, Appli
18	489	27.0	351	3	US-08-861-747-2	Sequence 2, Appli
19	488	27.0	351	3	US-08-789-982-2	Sequence 2, Appli
20	483.5	26.7	353	3	US-08-997-803-14	Sequence 14, Appli
21	437.5	24.2	509	2	US-08-845-566-1	Sequence 1, Appli
22	375	20.7	213	3	US-08-997-803-15	Sequence 15, Appli
23	365.5	20.2	393	2	US-08-467-948A-4	Sequence 4, Appli
24	365.5	20.2	393	3	US-08-467-947A-4	Sequence 4, Appli
25	357	19.7	360	1	US-08-671-525B-6	Sequence 6, Appli
26	357	19.7	360	1	US-08-672-109B-6	Sequence 6, Appli
27	357	19.7	360	2	US-08-842-045-6	Sequence 6, Appli



Qy 61 NSKPHSAMYFLGSLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120  
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Db 61 NSKPHSAMYFLGSLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120  
|||||  
Qy 121 GSLAIAIERVAIAKVKLYGSKSCRMILLIGASWLSISLVGLPILGWNCLHLEACS 180  
|||||  
Db 121 FSLAIAIERVAIAKVKLYGSKSCRMILLIGASWLSISLVGLPILGWNCLHLEACS 180  
|||||  
Qy 181 TVPLAKHYVLCVVTFISIIILAIYALYVRIYCVVSSHADMAAPQTLALKTVTVILG 240  
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Db 181 TVPLAKHYVLCVVTFISIIILAIYALYVRIYCVVSSHADMAAPQTLALKTVTVILG 240  
|||||  
Qy 241 VFICWLPAPFISILLDDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREV 300  
|||||  
Db 241 VFICWLPAPFISILLDDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREV 300  
|||||  
Qy 301 RPLQWRPGVGVQGRRRVGTGPHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353  
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Db 301 RPLQWRPGVGVQGRRRVGTGPHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353  
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## RESULT 2

US-09-760-936-2  
; -ence 2, Application us/08760936  
; ent No. 5856443  
; GENERAL INFORMATION:  
; APPLICANT: MacLennan, A. John  
; TITLE OF INVENTION: Molecular Cloning and Expression of  
; TITLE OF INVENTION: G-Protein Coupled Receptors  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08760.936  
; FILING DATE: December 6, 1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Doran R.  
; REGISTRATION NUMBER: 38,261  
; REFERENCE/DOCKET NUMBER: MAC-100C1  
; TELEPHONE: 352-375-8100  
; TELEFAX: 352-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-760-936-2

Query Match 87.8%; Score 1589.5; DB 2; Length 352;  
Best Local Similarity 88.7%; Pred. No. 1.1e-125;  
Matches 313; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MGSLYSEVLPNPKVQEHYNYTKETLETQETTSRQVASAGIVLCCAIWENLLVIAVAR 60  
|||||  
Db 1 MGSLYSEVLPNPKVQEHYNYTKETLETQETTSRQVASAGIVLCCAIWENLLVIAVAR 60  
|||||  
Qy 61 NSKPHSAMYFLGSLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120  
|||||

Db 61 NSKPHSAMYFLGSLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120  
|||||  
Qy 121 GSLAIAIERVAIAKVKLYGSKSCRMILLIGASWLSISLVGLPILGWNCLHLEACS 180  
|||||  
Db 121 FSLAIAIERVAIAKVKLYGSKSCRMILLIGASWLSISLVGLPILGWNCLHLEACS 180  
|||||  
Qy 181 TVPLAKHYVLCVVTFISIIILAIYALYVRIYCVVSSHADMAAPQTLALKTVTVILG 240  
|||||  
Db 181 TVPLAKHYVLCVVTFISIIILAIYALYVRIYCVVSSHADMAAPQTLALKTVTVILG 240  
|||||  
Qy 241 VFICWLPAPFISILLDDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREV 300  
|||||  
Db 241 VFICWLPAPFISILLDDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREV 300  
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Qy 301 RPLQWRPGVGVQGRRRVGTGPHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353  
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Db 301 RPLQWRPGVGVQGRRRVGTGPHLLPLRSSSSLERGHMPTSPTFLEGNTVV 353  
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## RESULT 3

US-08-196-989B-4  
; Sequence 4, Application US/08196989B  
; Patent No. 5585476  
; GENERAL INFORMATION:  
; APPLICANT: MacLennan, A. John  
; TITLE OF INVENTION: Molecular Cloning and Expression of  
; TITLE OF INVENTION: G-Protein Coupled Receptors  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08196.989B  
; FILING DATE: 15-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lloyd, Jeff  
; REGISTRATION NUMBER: 35,589  
; REFERENCE/DOCKET NUMBER: MAC-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 383 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-196-989B-4

Query Match 46.1%; Score 834; DB 1; Length 383;  
Best Local Similarity 48.4%; Pred. No. 2.1e-62;  
Matches 167; Conservative 60; Mismatches 104; Indels 14; Gaps 4;

Qy 3 SLYSEVLPNPKVQEHYNYTKETLETQETTSRQVASAGIVLCCAIWENLLVIAVAR 61  
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Db 15 SOVSQYGVNDIIVRHVNTYKLNIGVERDHGKILSVFILLICLLINIFVLLTIWT 74  
|||||  
Qy 62 SKPHSAMYFLGSLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 121  
|||||  
Db 75 KKHPRPMYFYIGNLALSDLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFVLSASF 134  
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Qy 122 SLLAIAIERVAIAKVKLYGSKSCRMILLIGASWLSISLVGLPILGWNCLHLEACS 181  
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Db 135 SLLAIAIERYITMLKMLHNGSNRSRFLISACWVLSLILGGLPIMGNCISSLSGST 194
QY 182 VLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS-----SHADMAAPOTLA 230
Db 195 VLPLYKHVILFCTVFTVTLILLISIVILYCRYSLVTRSRRLTFKKNISKASRSSEKSLA 254
QY 231 LKKTIVIGVFTVCMWLPAPFISILLDYACVPHSCPILYKAHYFFAVSTLNSLLNPVIYTW 290
Db 255 LKKTIVIVLSVETACWAPFLFILLDDVGCKAKTCDILYKAHYFLVLAVALNSGTNPVIYTL 314
QY 291 RSRDLREVLRLPLOCWR-PGVGVQGR-RRVGTGCHLLPLRSSSS 333
Db 315 TNKEMRRAFIRIISCCPCNGDSAGKFKRPIIPGMEFERSKSDNS 359

RESULT 5
US-08-845-566-3
; Sequence 3, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,566
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0271 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 181948
; US-08-845-566-3

```

```

Query Match 46.1%; Score 834; DB 2; Length 383;
Best Local Similarity 48.4%; Pred. No. 2.le-62;
Matches 167; Conservative 60; Mismatches 104; Indels 14; Gaps 4;

QY 3 SLYSEYLNPNKVOEHYNT-KETLETQETTSROVASAGIVILCCAVIENLLVIAVARN 61
Db 15 SOVSDYGNVDIIVRYHNTGKLNIGVEXDGIKLTSVVFLICCLILLENIFVLTWTKT 74
QY 62 SKFHSAVYFLGNLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASVG 121
Db 75 KKFHRPMYFYFIGNLALSLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFALSASF 134
QY 122 SLLAIAIERHVAIAKVKLYGCKSCRMILLIGASHLISLVILGGLPILGNCILGHLEACST 181
Db 135 SLLAIAIERYITMLKMLHNGSNRSRFLISACWVLSLILGGLPIMGNCISSLSGST 194

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QY 182 VLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS-----SHADMAAPOTLA 230
Db 195 VLPLYKHVILFCTVFTVTLILLISIVILYCRYSLVTRSRRLTFKKNISKASRSSEKSLA 254
QY 231 LKKTIVIGVFTVCMWLPAPFISILLDYACVPHSCPILYKAHYFFAVSTLNSLLNPVIYTW 290
Db 255 LKKTIVIVLSVETACWAPFLFILLDDVGCKAKTCDILYKAHYFLVLAVALNSGTNPVIYTL 314
QY 291 RSRDLREVLRLPLOCWR-PGVGVQGR-RRVGTGCHLLPLRSSSS 333
Db 315 TNKEMRRAFIRIISCCPCNGDSAGKFKRPIIPGMEFERSKSDNS 359

RESULT 5
US-08-845-566-3
; Sequence 3, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,566
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0271 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 181948
; US-08-845-566-3

```

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Query Match 45.5%; Score 823.5; DB 2; Length 381;
Best Local Similarity 49.7%; Pred. No. 1.5e-61;
Matches 156; Conservative 59; Mismatches 88; Indels 11; Gaps 2;

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QY 3 SLYSEYLNPNKVOEHYNT-KETLETQETTSROVASAGIVILCCAVIENLLVIAVARN 61
Db 14 SSVSDVYVDIIVRYHNTGKLNISADKENSIKLTSVFLICCLILENIFVLTWTKT 73
QY 62 SKFHSAVYFLGNLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASVG 121
Db 74 KKFHRPMYFYFIGNLALSLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFALSASF 133
QY 122 SLLAIAIERHVAIAKVKLYGCKSCRMILLIGASHLISLVILGGLPILGNCILGHLEACST 181

```



Patent No. 6090575  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, CRAMER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
~467-947A-28

Query Match 45.5%; Score 823.5; DB 3; Length 381;  
Best Local Similarity 49.7%; Pred. No. 1.5e-61;  
Matches 156; Conservative 59; Mismatches 88; Indels 11; Gaps 2;

QY 3 SLYSEYLNPNKVOEHNYT-KETLEQTTSRQVAGIVILCCAIYVENLLVIAVARN 61  
Db 14 SSVSDVYNDIIVRHNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKT 73  
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASVG 121  
Db 74 KKHPRMYFYIGNLALSDLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFVALSASF 133  
QY 122 SLAIAIERHVAIAKVKLYGCKSCRMILLIGASWLSILVGLGPILGWNCGLHLEACST 181  
Db 134 SLAIAIERYITMLKMKLHNGSNFRLLISACWVLSILGLGPIGWNCISALS SCSST 193  
QY 182 VLPLYAKHYVLCVVTTFISIIAIVAIYVRIYCVWRSSHADMA-----APOTLAL 231  
Db 194 VLPLYKHVILFCTVTFVTLISIVILYCRISLVRTSRRLTFRKNISKASRSSENVAL 253  
QY 232 LKTIVTLGVFVVCWLPAPFASILLDDYACPVHSPILYKAHYFVAVSTLNSLLNPVYTW 291  
Db 254 LKTIVTLVSVFIACWAPFLFILLDDVGCKVKTKDILFRAEYFLVAVLNSGTNPVITLT 313  
QY 292 SRDLREVLRPLQC 305

Db 314 NKEMRRAPIRMSC 327

## RESULT 9

PCT-US96-10618-4  
Sequence 4, Application PC/TUS9610618  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Guegler, Karl J.  
APPLICANT: Au-Young, Janice  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10618  
FILING DATE: 20-JUN-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,352  
FILING DATE: 20-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/567,817  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Glalster, Debra J.  
REGISTRATION NUMBER: 33,888  
REFERENCE/DOCKET NUMBER: PF-0042 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 119130  
PCT-US96-10618-4

Query Match 45.5%; Score 823.5; DB 5; Length 381;  
Best Local Similarity 49.7%; Pred. No. 1.5e-61;  
Matches 156; Conservative 59; Mismatches 88; Indels 11; Gaps 2;

QY 3 SLYSEYLNPNKVOEHNYT-KETLEQTTSRQVAGIVILCCAIYVENLLVIAVARN 61  
Db 14 SSVSDVYNDIIVRHNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKT 73  
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASVG 121  
Db 74 KKHPRMYFYIGNLALSDLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFVALSASF 133  
QY 122 SLAIAIERHVAIAKVKLYGCKSCRMILLIGASWLSILVGLGPILGWNCGLHLEACST 181  
Db 134 SLAIAIERYITMLKMKLHNGSNFRLLISACWVLSILGLGPIGWNCISALS SCSST 193

	Query Match	41.9%	Score 758;	DB 4;	Length 378;
	Best Local Similarity	47.5%;	Pred. No. 4.6e-56;		
	Matches 162; Conservative	55;	Mismatches 102;	Indels 22;	Gaps
Qy	14	VQEYNYT-----KETLETQETTSRQVASAGIVLICCAIVENLLVLTAIARNKFSH 66			
		: : : :           : : : :   : : : :   : : : :			
Db	18	LREHYQVVGKLGRKEASEGSTLT----TVLFVICSPVLENLVIAINKNKFHN 72			
Qy	67	ANYLFLGNLAASDLLAGVAFVNNTLLSGSVTLRTVPQWFAREGGSASITLSASVGSLLAI 126			
		: : :   : : :   : : :   : : :   : : :			
Db	73	RMYFFIGNLALCDLGIAYKNVILMSGKKTFSLSPTWELREGSMFVALGPCSLLAI 132			
Qy	127	AIERHVIAIKVKLVGSCSKSRMLLIGASWIIISVLVGLGPILGWNCIGHLEACSTVPLP 186			
		: : :   : : :   : : :   : : :   : : :			

Query Match	41.4%	Score 749;	DB 1;	Length 334;
Best Local Similarity	48.6%;	Pred. No. 2.3e-55;		
Matches 142;	Conservative 57;	Mismatches 81;	Indels 12;	Gaps
QY	35	VASAGIVILCCAIYVENLLVLIIVARNKSKHSAMYLFLGNLAASDLLIAGVAFVANTLLSG	94	
	:	: : : : : :	:	:
Dd	1	LTSVVFLICCFIIENIFVLLTWTKTKEPRHPMYEFGNIALSDLIAGVAYTANLLSG	60	
	:	: : : : : :	:	:
QY	95	SVTLRLPVQWFREGSASITLSVSQSLIAIATERHVATAKVLYGSCSRMLLIGA	154	
	:	: : : : : :	:	:
db	61	ATTYKLTAPQWFLREGSMFALSUSFSLSIAIATERYITMLKM-LHNGSNFRFLISA	119	
	:	: : : : : :	:	:

QY	155	SWLSISVLGGLPILGNWCLHLEACSTVLPYAKHYVL-CVWTIFSITLLAIVALXRVII	213
Db	120	CWISLILGGLPMGWNCISALSSTCVPLPYKHVYLFLCTLVFFILLLSIVILVCRII	179
QY	214	CVVRSSHADMA-----AQPTIALKTVTVILGVFICVLCPLAFSILLIDYACPVS	263
Db	180	SLVTRSRRLTFRKNISKASRSENALLKTVIIIVLSVFACWAPLFILLDLVDGCKVKT	239
QY	264	CPITYIAKHYEFAVYSTLNPNVIYTWSRSDLREVLRLQCWRPGVGQGR	315
Db	240	CDILFRAEFLVTAVINSQNPNIYTLTKNEKRAFIRIMCKPCSDGSAGK	291

RESULT 12  
 PCT-US93-08528-73  
 Sequence 73, Application PC/TUS9308528  
 GENERAL INFORMATION:  
 APPLICANT: New York University  
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
 NUMBER OF SEQUENCES: 348  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/08528  
 FILING DATE: 09-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/943,236  
 FILING DATE: 10-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Townsend, Kevin G.  
 REGISTRATION NUMBER: 34,033  
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 73:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 334 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US93-08528-73

Query Match 41.4%; Score 749; DB 5; Length 334;  
Best Local Similarity 48.6%; Pred. No. 2.3e-55;  
Matches 142; Conservative 57; Mismatches 81; Indels 12; Gaps 3;

Qy	35	VASAGVILCAITWENLLVLI	AVARNRSKFHSAMYFLGNLAASDILAGVAFVANTLLSG	94	
		:	:	:	
Db	1	LTSWFLICCFIL	ENIFVLLTIWTKFHRPMYFIGNIALSDIAGVATANLLSG	60	
		:	:	:	
Qy	95	SVTLRLTPQWFAR	SGASITISASVGSLLAIAIERHVAIAKVLKYGCSKRMILLICA	154	
		:	:	:	
Db	61	ATTYKLTPAQWFL	REGSMFVSLSVFSLAIAERYITMLKM-LHNGSNRFLFLICA	119	
		:	:	:	
Qy	155	SWLSISVLGGLPTL	GNWCLGHLEACTVLPVLAKHVVL-CVVTIISIILAI	213	
		:	:	:	
Db	120	CWVISILGGLPL	MGNWCISALS	CSCTVPLVKKHVFELCTIVTLFVLLSVILYCRY	179
		:	:	:	

Query Match	29.1%	Score 526;	DB 5;	Length 393;
Best Local Similarity	35.7%	Pred. No. 1.3e-36;		
Matches 121				

	Matches	121;	Conservative	70;	Mismatches	116;	Indels	32;	Gaps	10;
QY	18	YNYTKETLEQ-ERTSRQVASAGVIILCCAIWENLLVLIIVARNSKPFSAMYLFLGNLA	76	: :	: :	: :	: :	:	:	
Db	34	YNRSCKLYATEWNTSVKLVMLGTLTV-CIFIMLANLLVMVAIYNRRRFFFIYYLMA NLA	92	:	: :	: :	: :	:	:	
QY	77	ASDLLAGVAFVANITLLSGSVTLRLTPTQWFARQSASITLSASVGSLLAIAIERHVAIK	136	:    :    :    :	:    :    :    :	:    :    :    :	:	:	:	

Db 93 AADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLDITVTASVANLLAIAIERHITVER 152

Qy 137 VKLVGSKSCRMILLIGASWLSIVLGLPILGWNCLHLEACSTVPLPYAKHYVLCVVT 196

Db 153 MOLHTRMSNRVVVVVITWTAIVMGAIPTSVGWNICIDHCNSNMAPLYSDSY-LVFWA 211

Qy 197 IFSII-LIAIVALYVRIYCVVR-----SSHADMAPO-----TLALLKTVIIVLGVFIV 244

Db 212 IFNLVTFVVMVVLVAHIFGYVQRTMRMSRHS--SGPRNRDRTMMSLLKTVIIVLGAFLI 269

Qy 245 CWLPAFSLILLDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVLRLPQ 304

Db 270 CWTGCLVLLLDVCCP--QCDVLAYPEKFFLLAEFNSAMNPIIYSYRDKEMSATFRQILC 327

Qy 305 CWRPGVGVQRRRVGTPGHLLPLRSSSSLER-----GMH 339

Db 328 C-----QRSENTSGTSGRSDRSASSLNHTILAGVH 357

RESULT 14

US-08-763-938-2

Sequence 2, Application US/08763938

Pat No. 6140060

GENERAL INFORMATION:

APPLICANT: CHUN, Jerold J.M.

APPLICANT: HECHT, Jonathan H.

TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID

TITLE OF INVENTION: RECEPTORS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP

STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/763,938

FILING DATE: 12-DEC-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: JAHNS, Kristina M.

REGISTRATION NUMBER: 41,092

REFERENCE/DOCKET NUMBER: P8074-6018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-5000

TELEFAX: (202) 638-4810

FORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-763-938-2

Query Match 28.9%; Score 523; DB 4; Length 364;

Best Local Similarity 35.7%; Pred. No. 2.le-36;

Matches 116; Conservative 71; Mismatches 116; Indels 22; Gaps 9;

Qy 18 YNYTKETLETO-ETTSQVAGSIVILCCAVENLLVLAIVARNKFSAMVLFGLNLA 76

Db 34 YNRSGLATEWNTSKVLMGLITV-CVFIMLANLLVMVAIYVNRFRFPFIYLMANLA 92

Qy 77 ASDLLAGVAFVANTLLSGSVTLRLTPVQWFARECSASITLSASVGSLLATAIERHVAIAK 136

Db 93 AADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLDITVTASVANLLAIAIERHITVER 152

Qy 137 VKLVGSKSCRMILLIGASWLSIVLGLPILGWNCLHLEACSTVPLPYAKHYVLCVVT 196

Db 153 MOLHTRMSNRVVVVVITWTAIVMGAIPTSVGWNICIDHCNSNMAPLYSDSY-LVFWA 211

Qy 197 IFSII-LIAIVALYVRIYCVVR-----SSHADMAPO-----TLALLKTVIIVLGVFIV 244

Db 212 IFNLVTFVVMVVLVAHIFGYVQRTMRMSRHS--SGPRNRDRTMMSLLKTVIIVLGAFLI 269

Qy 245 CWLPAFSLILLDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVLRLPQ 304

Db 270 CWTGCLVLLLDVCCP--QCDVLAYPEKFFLLAEFNSAMNPIIYSYRDKEMSATFRQILC 327

Qy 305 CWRPGVGVQRRRVGTPGHLL 326

Db 328 CORNENPNGPTGSDRSASSLNHTI 352

RESULT 15

PCT-US96-10618-2

Sequence 2, Application PC/TUS9610618

GENERAL INFORMATION:

APPLICANT: Coleman, Roger

APPLICANT: Guegler, Karl J.

APPLICANT: Au-Young, Janice

APPLICANT: Bandman, Olga

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10618

FILING DATE: 20-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,352

FILING DATE: 20-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/567,817

FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Glaister, Dendra J.

REGISTRATION NUMBER: 33,888

REFERENCE/DOCKET NUMBER: PF-0042 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: Rheumatoid Synovium

CLONE: 80853

PCT-US96-10618-2

Query Match 28.9%; Score 523; DB 5; Length 364;

Best Local Similarity 35.7%; Pred. No. 2.le-36;  
Matches 116; Conservative 71; Mismatches 116; Indels 22; Gaps 9;

QY	18	YNYTKETLEQ-ETTSROVASAGIVILCCAIWENLLVLIIVARNRKFHSAWYFLGNLA	76
Db	34	YNRSGKHLATEWNTVSKLVWCLGTV-CIFIMLANLLVMVAIYVNRFRFFIYYLMA	92
QY	77	ASDLLACVAFVANTLLSGSVTLRLTPVQWFAREGSASTLSASVGSLLAIAIERHVAIAK	136
Db	93	AADFFAGLAYFYLMFNTGPNTRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFR	152
QY	137	VKLYGCKSCRMULLIGASWLSIVLGLPLTILGNCLHLEACSTVPLPIAKHYVLCVVT	196
Db	153	MLHTRMSNRVVVIVVITMAIVMGAIPSVGNWCIDICNSMAPLYSDSY-LVFWA	211
QY	197	IFSII-LLAIVALYVRIYCVVR-----SSHADMAAPQ-----TLALKTVTIVLGVFIV	244
D'	212	IFNLVTFVVMVLYAHIFGVYRQRTMRMSRHS--SGPRNRDTHMSLLKTVVIVLGGFII	269
QY	245	CWLPAPFILLDDYACPVHSCPILYKAHYFAVSTLNSLLNPVIYTWRSRDLRREVLRLPQ	304
Db	270	CWTPGLVLLLDVCCP--QCDVLAYEKFFLLAEFNSAMNPITYSYRDKEMSAFRLIC	327
QY	305	CWR---PGVGVQGRRRVGTPECHLL	326
Db	328	QRSENPTAPTEGSDRSASSLNHTI	352

Search completed: December 20, 2001, 10:46:09  
Job time: 2218 sec



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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-861-747-3

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Query Match	96.9%	Score 1680;	DB 3:	Length 1889;
Best. Local Similarity	98.7%	Pred. NO. 0;		
Matches 1703;	Conservative	1;	Mismatches 21;	Indels 1

1

[illegible]

Qy	902	tcttggtgtgagaaagtacttcttactgtgtgccgagcccaactcacttggtcaatgctg	961
Db	994	TCCTGGCTGTAGAAAAGTACTTCCCTACTCTTGGCGAGGCCAACTCAGTGGTCAATGCTG	1053
Qy	962	ctgtactacttgcgagatgctgagatgcgcgcacacttccgcgcgccttctctgtcgtcg	1021
Db	1034	CTGTGTACTTTCGCGAGATGCTGAGATGCGCGCACCTTCGCGCCCTTCTCTGCTGCG	1113
Qy	1022	ctgtctccgcagtcacaccgcgagctctgtccactatatacttctctgcgcaggaggtg	1081
Db	1114	CGTGCTCCGCCAGCCACCCGCGAGTCTGTCCACTATACATCTCTGCCAGGGAGGTG	1173
Qy	1092	ccagcaactgcatactgtctcccgagaacggccacccactgat-gactccacccctttagc	1140
Db	1174	CCAGCACTCGCATCATGCTTCCGAGAACGGCCACCCACTGATGAGCTCCACCCCTTAGC	1233
Qy	1141	tacctgaacttcagcggtagcggcaagcaacaataccagacccctgatgacttgtgg	1200
Db	1234	TACCTTGAACCTCAGCGGTACGGCGCAGCAACAATCCACGCCCTTGATGACTTGTGG	1293
Qy	1201	gtgtctctgggtcaaccccaacacaggaactgactggtgcaggacaaggtcttggcatg	1260
Db	1294	GTGTCTCTGGCTCAACCCAACACAGGACTGACTACCGCGCAGCACAAAGGTCTGCATG	1353
Qy	1261	gcacagcacactaccaggtctcccaaggcacacacactctgcgcagggaatggggcttt	1320
Db	1354	GCACAGACCACCTGCCAGGCTCCCCAGGCACACCACCTCTGCCCAGGGAATGGGGCTTT	1413
Qy	1321	gggtcatctcccaactgcctggggagtcagatgggggtcagggaactcgtgctcttcagcca	1380
Db	1414	GGGTCACTCCCACTGCTTGGGGAGTCAGATGGGGTCAGAGAACTGGCTCTTCAGCCA	1473
Qy	1381	tctcaggttagggggtttgtaacagacattattctgttttcactgcgtatccttggtaa	1440
Db	1474	TCCCAGGTTTAGGGGGTTTGTAAACAGACATTATTCTGTTTTCACTGCGTATCTTGGTAA	1533
Qy	1441	gccctgtggactggttaatgctgtgtgatcgtgaggttttaaggctggggagagataagg	1500
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Qy	1501	gctctctgggccaatgctacccggtagactgggttaatgaggacagactgtggacacccc	1560
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RESULT 2

US-08-760-936-2

Sequence 2, Application US/08760936

Patent No. 5856443

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760.936

FILING DATE: December 6, 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Doran R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: MAC-100C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-760-936-2

Query Match 87.8%; Score 1589.5; DB 2; Length 352;  
Best Local Similarity 88.7%; Pred. No. 1.1e-125;  
Matches 313; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

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Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

wed n.

Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSASITLSASV 120  
Qy 121 GSLLAIAIERHVAIAKVKLYGCKSCRMMLLIGASWLISLVLGGPLILGNWCLGHLEACS 180  
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RESULT 3

US-08-196-989B-4

1400

Wed

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Best Local Similarity	82.2%	Pred. No. 1.4e-146;		
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Db	403	TTCGTGGCCAACACCTTGCTCTCCGACCTGTCAACCTGTCTTAACCTCCCTGCAGTGG	462
Qy	376	tttgcccgaggagggctctgctccatcacgctctcggcctctgtcttcagcctcctggcc	435
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Qy	436	atcgccattgagcgccacgtggccattgccaagggtcaagctgtatggcagcgacaagagc	495
Db	523	ATTGCCATCGAGAGACAAGTGGCCATCGCCAAGGTCAAGCTCTACGGCAGTGACAAAAGC	582
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Qy	556	cccatccttggttggaactgcctggggccacctcgaggctgctccactgtcctgcctctc	615
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Qy	616	tacgccaagcattatgtgtgtgctgtgacctcttctccatcatcctgttggccatc	675
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Wed Dec 26 09:32:47 2001

us-09-274

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RESULT 3  
US-09-00000000  
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## ALIGNMENTS

RESULT : 1  
 US-08-861-747-1  
 ; Sequence 1, Application US/08861747  
 ; Patent No. 6020158  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MUNROE, Donald G.  
 ; APPLICANT: VYAS, Tejal B.  
 ; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
 ; STREET: 655 15th St., NW, Suite 330 - G Street Lobby  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-5701  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/861,747  
 ; FILING DATE: 22-MAY-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jahns, Kristina M.  
 ; REGISTRATION NUMBER: 41,092  
 ; REFERENCE/DOCKET NUMBER: P8074-7003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 638-5000  
 ; TELEFAX: (202) 638-4810  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1761 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-08-861-747-1

Query Match 96.9%; Score 1680; DB 3; Length 1761;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 1703; Conservative 1; Mismatches 21; Indels 1; Gaps 1;

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RESULT 2  
US-08-861-747-3  
Sequence 3, Application US/08861747  
Patent No. 6020158  
GENERAL INFORMATION:  
APPLICANT: MUNROE, Donald G.  
APPLICANT: VYAS, Tejal B.  
TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
STREET: 655 15th St., NW, Suite 330 - G Street Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,747  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Jahns, Kristina M.  
REGISTRATION NUMBER: 41, 092  
REFERENCE/DOCKET NUMBER: P8074-7003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 3:

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seq_documentation_block:
; Sequence 1, Application US/08861747
; Patent No. 6020158
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1761 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-861-747-1
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Quality: 1941.00      Length: 383
Ratio: 5.094          Gaps: 1
Percent Similarity: 99.478  Percent Identity: 98.956
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34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
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184 euLeuSerArgSerTyrLeuAlaValAlaValAlaLeuSerSerLeuVal 200
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; Patent No. 6020158
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VIAS, Tejal B.
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
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DEFINITION Homo sapiens G protein-coupled receptor Eag-4 mRNA, complete cds.  
ACCESSION AF011466  
VERSION AF011466.1 GI:2735848  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM

REFERENCE 1 (bases 1 to 1734)  
AUTHORS An.S., Bleu.T., Hallmark.O.G. and Goetzl.E.J.  
TITLE Characterization of a novel subtype of human G protein-coupled receptor for lysophosphatidic acid  
J. Biol. Chem. 273 (14), 7906-7910 (1998)  
MEDLINE 98192573  
REFERENCE 2 (bases 1 to 1734)  
AUTHORS An.S.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-1997) Medicine, UCSF, 533 Parnassus Ave., Rm U08, San Francisco, CA 94143-0711, USA  
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VERSION     AF011466.1 GI:2735848
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ORGANISM    Homo sapiens
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REFERENCE   1 (bases 1 to 1734)
AUTHORS     An.S., Bleu,R., Hallmark,O.G. and Goetzl,E.J.
TITLE       Characterization of a novel subtype of human G protein-coupled
JOURNAL     receptor for lysophosphatidic acid
MEDLINE     J. Biol. Chem. 273 (14), 7906-7910 (1998)
REFERENCE   2 (bases 1 to 1734)
AUTHORS     An.S.
TITLE       Direct Submission
JOURNAL     Submitted (28-JUN-1997) Medicine, UCSF, 533 Parnassus Ave., Rm Ub8,
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AUTHORS    MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.
TITLE      Cloning and characterization of a putative G-protein coupled
             receptor potentially involved in development
JOURNAL     Mol. Cell. Neurosci. 5 (3), 201-209 (1994)
MEDLINE     94373324
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AUTHORS    An,S.
TITLE      Edg5, a Human homolog of rat H218 that is a functional receptor for
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JOURNAL     Unpublished
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AUTHORS    An,S.
TITLE      Direct Submission
JOURNAL     Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
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184 roLeuTyrAlaLysHisTyrValLeuCysValValThrIlePheSerI 200  
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551 CTCTCTACGCCAAGCATATTGTGTGTGGTGGTGACCATCTCTCCATC 600  
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201 IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValVal 217  
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601 ATCTGTGTGGCCATCTGTGGCCCTGTAGCTGCGCATCTACTGCTGTCG 650  
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217 gSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLys 234  
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651 CTCAGCCACGCTGACATGGCCGCCCGCCAGACGCTAGCCCTGCTCAAGA 700  
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234 hrValThrIleValLeuGlyValPheIleValCysTrpLeuProAlaP 250  
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701 CGGTACCATCTGCTAGGCTCTTTATCTGCTGCTGGCTGCCGCCCTTC 750  
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251 SerIleLeuLeuLeuAspTyrAlaCysProValHisSerCysProIle 267  
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751 AGCATCTCTCTTGGACTATGCTGTCCGCTCCACTCTCTGCCGATCCT 800  
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267 uTyrLysAlaHisTyrPheAlaValSerThrLeuAsnSerLeuLeu 284  
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801 CTACAAGCCCATCTACTTTTCGCCGTCTCCACCTGAATTCCTGCTCA 850  
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284 snProValIleTyrThrTrpArgSerArgAspLeuArgGluValLeu 300  
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851 ACCCCGTCACTACATGTGGCGAGCGGGACCTGCGGGGAGGTGCTT 900  
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301 ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArg 317  
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317 gValGlyThrProGlyHisHisLeuLeuProLeuArgSerSerSerL 334  
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951 GGTCCGAGCCCGGGCCACACCTCTGTCCACTCCGACGCTCCAGCTCC 1000  
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334 euGluArgGlyMetHisMetProThrSerProThrPheLeuGluGlyAsn 350  
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1001 TGGAGAGGGGCATGCACATGCCACGTCACCCACGTTTCTGGAGGGCAAC 1050  
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351 ThrValVal 353  
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1051 ACGGTGGTC 1059  
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# ALIGNMENTS

RESULT 1  
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 LOCUS AF034780 1062 bp mRNA PRI 01-JAN-1999  
 DEFINITION Homo sapiens lysosphingolipid receptor Edg5 mRNA, complete cds.  
 ACCESSION AF034780  
 VERSION AF034780.1 GI:4090955  
 KEYWORDS  
 SOURCE human.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1062)  
 AUTHORS MacLennan, A.J., Browe, C.S., Gaskin, A.A., Lado, D.C. and Shaw, G.  
 TITLE Cloning and characterization of a putative G-protein coupled  
 receptor potentially involved in development  
 JOURNAL Mol. Cell. Neurosci. 5 (3), 201-209 (1994)  
 MEDLINE 94373324  
 REFERENCE 2 (bases 1 to 1062)  
 AUTHORS An, S.  
 TITLE Edg5, a Human homolog of rat H218 that is a functional receptor for

lysophingolipids  
Unpublished  
REFERENCE 3 (bases 1 to 1062)  
AUTHORS An.S.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus  
Ave., San Francisco, CA 94143-0711, USA  
FEATURES  
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BASE COUNT 166 a 367 c 294 g 235 t  
ORIGIN

Query Match 88.1%; Score 988.8; DB 9; Length 1062;  
Best Local Similarity 94.5%; Pred. No. 6.4e-162;  
Matches 1060; Conservative 0; Mismatches 2; Indels 60; Gaps 1;  
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Db 1 ATGGGCAGCTTGACTCGGAGTACCTGAAACCCCAACAGGTCCAGGAACACTAATAT 60  
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QY 121 gtcactctctgttgcacatgcaggagagacacctcccgagggtggtcccttcac 180  
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